

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Innogenetics sa.
- (B) STREET: Industriepark Zwijnaarde 7, box 4
- (C) CITY: Ghent
- (E) COUNTRY: Belgium
- (F) POSTAL CODE (ZIP): B-9052
- (G) TELEPHONE: 00 32 9 241 07 11
- (H) TELEFAX: 00 32 9 241 07 99

(ii) TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy.

(iii) NUMBER OF SEQUENCES: 270

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR34-4-20

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTC ACG GAA CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG
 Leu Thr Glu Arg Leu Tyr Cys Gly-Gly Pro Met Phe Asn Ser Lys Gly
 1 5 10 15

48

GCC CAG TGT GGT TAT CGC CGC TGC CGT GCC AGT GGA GTT CTG CCT ACC
 Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr

96

20	25	96	30	
AGC TTC GGC AAC ACA ATC ACT TGC TAC ATC AAG GCC ACA GCG GCT GCA Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala				144
35	40		45	
AGG GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTC TGC GGA GAT GAT Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp				192
50	55		60	
CTG GTC GTG GTG GCT GAG AGT Leu Val Val Val Ala Glu Ser				213
65	70			

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Leu	Thr	Glu	Arg	Leu	Tyr	Cys	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly
1				5					10					15	
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr															
				20				25					30		
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala															
				35				40					45		
Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp															
				50				55					60		
Leu Val Val Val Ala Glu Ser															
				65				70							

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR36-23-18

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTC ACG GAA CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG	48
Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly	
1 5 10 15	
GCC CAG TGT GGT TAT CGC CGC TGC CGT GCC AGT GGA GTT CTG CCT ACC	96
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr	
20 25 30	
AGC TTC GGC AAC ACA ATC ACT TGC TAC ATC AAG GCC ACA GCG GCT GCA	144
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala	
35 40 45	
AGG GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTC TGC GGA GAT GAT	192
Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp	
50 55 60	
CTG GTC GTG GTG GCT GAG AGT	213
Leu Val Val Val Ala Glu Ser	
65 70	

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly	
1 5 10 15	
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr	
20 25 30	
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala	
35 40 45	
Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp	
50 55 60	
Leu Val Val Val Ala Glu Ser	
65 70	

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-23-18

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTT AAC AGC AAG GGG
 Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
 1 5 10 15

48

GCC CAG TGT GGT TAT CGC CGT TGC CGT GCC AGT GGA GTT CTG CCT ACC
 Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
 20 25 30

96

AGC TTC GGC AAC ACA ATC ACT TGT TAC ATC AAA GCC ACA GCG GCC GCA
 Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
 35 40 45

144

AAA GCC GCA GGC CTC CGG AGC CCG GAC TTT CTT GTC TGC GGA GAT GAT
 Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp
 50 55 60

192

CTG GTC GTG GTG GCT GAG AGT
 Leu Val Val Val Ala Glu Ser
 65 70

213

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
 1 5 10 15

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
 20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
 35 40 45

99

Lys	Ala	Ala	Gly	Leu	Arg	Ser	Pro	Asp	Phe	Leu	Val	Cys	Gly	Asp	Asp
50							55					60			

Leu	Val	Val	Val	Ala	Glu	Ser
65				70		

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR36-23-20

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTC	ACG	GAG	CGG	CTT	TAC	TGC	GGG	GGC	CCT	ATG	TTT	AAC	AGC	AAA	GGG	
Leu	Thr	Glu	Arg	Leu	Tyr	Cys	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly	
1				5					10				15			48

GCC	CAG	TGT	GGT	TAT	CGC	CGT	TGC	CGT	GCC	AGT	GGA	GTT	CTG	CCT	ACC	
Ala	Gln	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Pro	Thr	
				20					25				30			96

AGC	TTC	GGC	AAC	ACA	ATC	ACT	TGT	TAC	ATC	AAA	GCC	ACA	GCG	GCC	GCA	
Ser	Phe	Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Ile	Lys	Ala	Thr	Ala	Ala	Ala	
				35					40				45			144

AAA	GCC	GCA	GGC	CTC	CGG	AGC	CCG	GAC	TTT	CTT	GTC	TGC	GGA	GAT	GAT	
Lys	Ala	Ala	Gly	Leu	Arg	Ser	Pro	Asp	Phe	Leu	Val	Cys	Gly	Asp	Asp	
				50					55			60				192

CTG	GTC	GTG	GTG	GCT	GAG	AGT										213
Leu	Val	Val	Val	Ala	Glu	Ser										
65				70												

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

100

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
 1 5 10 15

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
 20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
 35 40 45

Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp
 50 55 60

Leu Val Val Val Ala Glu Ser
 65 70

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR33-2-17

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG 48
 Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
 1 5 10 15

GCC CAG TGT GGT TAT CGC CGT TGT CGT GCC AGT GGA GTT CTG CCT ACC 96
 Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
 20 25 30

AGT TTC GGC AAC ACA ATC ACT TGT TAC ATC AAG GCC ACA GCG GCT GCA 144
 Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
 35 40 45

AAA GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTT TGC GGA GAT GAT 192

101

Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp
50 55 60

TTG GTC GTG GTG GCT GAG AGT
Leu Val Val Val Ala Glu Ser
65 70

213

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
1 5 10 15

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
35 40 45

Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp
50 55 60

Leu Val Val Val Ala Glu Ser
65 70

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: BR33-2-21

(ix) FEATURE:
(A) NAME/KEY: CDS -
(B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly 1 5 10 15	48
GCC CAG TGT TAT CGC CGT TGT CGT GCC AGT GGA GTT CTG CCT ACC Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr 20 25 30	96
AGT TTC GGC AAC ACA ATC ACT TGT TAC ATC AAG GCC ACA GCG GCT GCA Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 35 40 45	144
AAA GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTT TGC GGA GAT GAT Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp 50 55 60	192
TTG GTC GTG GTG GCT GAG AGT Leu Val Val Val Ala Glu Ser 65 70	213

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly 1 5 10 15
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr 20 25 30
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 35 40 45
Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp 50 55 60
Leu Val Val Val Ala Glu Ser 65 70

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-2-5

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	46
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	94
20 25 30	
GGT TGC TCC TTT TCT ATC TTC CTT GCT CTG TTC TCT TGC TTA ATC Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	142
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAC ACG TCT GGC CTC TAT GTC His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	190
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	238
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGT AAT Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	286
80 85 90 95	
ACA TCT GCG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AGG TAC Thr Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	334
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATG TTG GTG Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Met Leu Val	382
115 120 125	
GGC GCG GCC ACG ATG TGC TCT GCT CTC TAC GTG GGT GAT ATG TGT GGG Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	430
130 135 140	
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	478
145 150 155	
CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser	526
160 165 170 175	

GGA CAC CGA ATG GCT
 Gly His Arg Met Ala
 180

541

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val
 1 5 10 15

Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly
 20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His
 35 40 45

Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
 50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val
 65 70 75 80
 Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr
 85 90 95

Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
 100 105 110

Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Met Leu Val Gly
 115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala
 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
 165 170 175

His Arg Met Ala
 180

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 541 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

05906070-07060500-00000000

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-2-14

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATC TTC CTT CCT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Pro Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAC ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGT AAT	286
Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCT GCG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AGG TAC	334
Thr Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATA TTG GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val	
115 120 125	
GGC GCG GCC ACA ATG TGC TCT GCT CTC TAC GTG GGT GAT ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT	478
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	
145 150 155	
CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA	526

Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser
 160 165 170 175

GGA CAC CGA ATG GCT
 Gly His Arg Met Ala 541
 180

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val
 1 5 10 15

Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly
 20 25 30

Cys Ser Phe Ser Ile Phe Leu Pro Ala Leu Phe Ser Cys Leu Ile His
 35 40 45

Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
 50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val
 65 70 75 80

Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr
 85 90 95

Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
 100 105 110

Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val Gly
 115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala
 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
 165 170 175

His Arg Met Ala
 180

(2) INFORMATION FOR SEQ ID NO: 17 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 541 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-2-21

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATC TTC CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAC ACG TCT GGC CTC TAC GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGT AAT	286
Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCT GCG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AGG TAC	334
Thr Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATA TTG GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val	
115 120 125	
GGC GCG GCC ACG ATG TGC TCT GCT CTC TAC GTG GGT GAT ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	

GCC GTC TTC CTC GTG GGA CAA GCC	TTC ACG TTC AGA CCT CGT CGC CAT	478
Ala Val Phe Leu Val Gly Gln Ala	Phe Thr Phe Arg Pro Arg Arg His	
145	150	155
CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA		526
Gln Thr Val Gln Thr Cys Asn Cys Ser	Leu Tyr Pro Gly His Leu Ser	
160	165	170
GGA CAC CGA ATG GCT		
Gly His Arg Met Ala		541
180		

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val			
1	5	10	15
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly			
20	25	30	
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His			
35	40	45	
Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu			
50	55	60	
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val			
65	70	75	80
Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr			
85	90	95	
Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val			
100	105	110	
Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val Gly			
115	120	125	
Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala			
130	135	140	
Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln			
145	150	155	160
Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly			
165	170	175	
His Arg Met Ala			

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR36-9-13

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	46
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	94
20 25 30	
GGT TGC TCC TTT TCT ATT TTC CTT CTT GCT CTG TTC TCT TGC TTA ATT Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	142
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	190
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAC GAG GCC GAT GAC Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	238
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGC ATA CCT TGT GTC CAG GAC GGC AAT Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn	286
80 85 90 95	
ACA TCC ACG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AAG TAC Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr	334
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val	382
115 120 125	

GGC GCG GCC ACG ATG TGC TCA GCG CTC TAC GTG GGT GAT ATG TGT GGG Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly 130 135 140	430
GCC GTC TTC CTT GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His 145 150 155	478
CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser 160 165 170 175	526
GGA CAT CGA ATG GCT Gly His Arg Met Ala 180	541

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val 1 5 10 15
--

Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly 20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His 35 40 45

Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80
--

Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn Thr 85 90 95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr Val 100 105 110
--

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly 115 120 125
--

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala 130 135 140
--

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln 145 150 155 160
--

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly

165

170

175

His Arg Met Ala
180

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR36-9-20

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATT TTC CTT GCT CTG TTC TCT TGC TTA ATT	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAC GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGC ATA CCT TGT GTC CAG GAC GGC AAT	286
Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCC ACG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AAG TAC	334
Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr	
100 105 110	

GTC GGA GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val 115 120 125	382
GGC GCG GCC ACG ATG TGC TCT GCG CTC TAC GTG GGT GAC ATG TGT GGG Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly 130 135 140	430
GCT GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His 145 150 155	478
CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser 160 165 170 175	526
GGA CAT CGA ATG GCT Gly His Arg Met Ala 180	541

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val 1 5 10 15
--

Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly 20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His 35 40 45

Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80
--

Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn Thr 85 90 95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr Val 100 105 110
--

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly 115 120 - 125
--

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala 130 135 140
--

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
 165 170 175

His Arg Met Ala
 180

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 541 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR33-1-10

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	

TGT AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	

GGT TGC TCC TTT TCT ATC TTC CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	

CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	

CTT ACC AAC GAC TGT TCC AAT AGT AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	

GTT ATT CTG CAC GCG CCC GGC TGT GTA CCT TGT GTC CAG GAC GGC AAT	286
Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	

ACG TCT ACA TGC TGG ACC CCA GTA ACA CCT ACA GTG GCA GTC AGG TAC Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr 100 105 110	334
GTC GGG GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTG TTA GTA Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val 115 120 125	382
GGC GCG GCC ACG ATG TGC TCT GCG CTT TAC GTG GGT GAT ATG TGT GGG Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly 130 135 140	430
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCC CGC CGC CAT Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His 145 150 155	478
CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser 160 165 170 175	526
GGA CAT CGC ATG GCT Gly His Arg Met Ala 180	541

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val
1 5 10 15

Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly
20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His
35 40 45

Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val
65 70 75 80

Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr
85 90 95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
100 105 110

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly

115	120	125
Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala		
130	135	140
Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln		
145	150	155
160		
Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly		
165	170	175
His Arg Met Ala		
180		

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR33-1-19

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46		
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly			
1	5	10	15
GTG AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC	94		
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro			
20	25	30	
GGT TGC TCT TTT TCT ATC TTC CTT GCT CTG TTC TCT TGC TTA ATC	142		
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile			
35	40	45	
CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190		
His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val			
50	55	60	
CTT ACC AAC GAC TGT TCC AAT AGT AGT ATT GTG TAT GAG GCC GAT GAC	238		
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp			
65	70	75	

GTT ATT CTG CAC GCG CCC GGC TGT GTA CCT TGT GTC CAG GAC GGC AAT Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn 80 85 90 95	286
ACG TCT ACA TGC TGG ACC CCA GTA ACA CCT ACA GTG GCA GTC AGG TAC Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr 100 105 110	334
GTC GGG GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTG TTA GTA Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val 115 120 125	382
GGC GCG GCC ACG ATG TGC TCT GCG CTT TAC GTG GGT GAT ATG TGT GGG Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly 130 135 140	430
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCC CGC CGC CAT Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His 145 150 155	478
CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser 160 165 170 175	526
GGA CAT CGA ATG GCT Gly His Arg Met Ala 180	541

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val 1 5 10 15
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly 20 25 30
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His 35 40 45
Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50 55 60
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80
Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr 85 90 95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
 100 105 110

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly
 115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala
 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
 165 170 175

His Arg Met Ala
 180

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR33-1-20

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC 46
 Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 1 5 10 15

GTC AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC 94
 Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro
 20 25 30

GGT TGC TCT TTT TCT ATC TTC CTT GCT CTG TTC TCT TGC TTA ATC 142
 Gly Cys Ser Phe Ser Ile Phe Leu Ala Leu Phe Ser Cys Leu Ile
 35 40 45

CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC 190
 His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val
 50 55 60

CTT ACC AAC GAC TGT TCC AAT AGT AGT ATT GTG TAT GAG GCC GAT GAC		238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp		
65	70	75
GTT ATT CTG CAC GCG CCC GGC TGT GTA CCT TGT GTC CAG GAC GGC AAT		286
Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn		
80	85	90
95		
ACG TCT ACA TGC TGG ACC CCA GTA ACA CCT ACA GTG GCA GTC AGG TAC		334
Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr		
100	105	110
GTC GGG GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTG TTA GTA		382
Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val		
115	120	125
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly		
130	135	140
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCC CGC CGC CAT		430
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His		
145	150	155
CAT		
CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA		526
Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser		
160	165	170
175		
GGA CAT CGA ATG GCT		541
Gly His Arg Met Ala		
180		

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val
      1           5           10          15
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly
      20          25          30

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Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His
35 40 45

Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val
65 70 75 80

Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr
 85 90 95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
 100 105 110

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly
 115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala
 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
 165 170 175

His Arg Met Ala
 180

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 287 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HCC1153

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 3..287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TA GAC TTT TGG GAG AGC GTC TTC ACT GGA CTA ACT CAC ATA GAT GCC	47
Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala	
1 5 10 15	
CAC TTT CTG TCA CAG ACT AAG CAG CAG GGA CTC AAC TTC TCG TTC CTG	95
His Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu	
20 25 30	
ACT GCC TAC CAA GCC ACT GTG TGC GCT CGC GCG CAG GCT CCT CCC CCA	143
Thr Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro	
35 40 45	
AGT TGG GAC GAG ATG TGG AAG TGT CTC GTA CGG CTT AAG CCA ACA CTA	191

Ser Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu
 50 55 60

CAT GGA CCT ACG CCT CTT CTA TAT CGG TTG GGG CCT GTC CAA AAT GAA 239
 His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu
 65 70 75

ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG GCA TGC ATG TCA 287
 Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser
 80 85 90 95

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His
 1 5 10 15

Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu Thr
 20 25 30

Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser
 35 40 45

Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu His
 50 55 60

Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile
 65 70 75 80

Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser
 85 90 95

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HD10-1-25

09399016 - 070601

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC GTC ACA AAA TAC ATT ATG Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met	47
1 5 10 15	
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTG TTG Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu	95
20 25 30	
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGC Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly	143
35 40 45	
TGC GTT GTA ATC GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA CTC Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu	191
50 55 60	
GTT CCA GAC AAG GAG GTG TTG TAT CAA CAG TAC GAT GAG ATG GAG GAG Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu	239
65 70 75	
TGC TCG CAA GCC GCC CCA TAC ATC GAA CAA GCT CAG GTA ATA GCC CAC Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His	287
80 85 90 95	
CAG TTC AAG GAG AAA ATC CTT GGA CTG CTG CAG CGA GCC ACC CAA CAA Gln Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln	335
100 105 110	
CAA GCT GTC ATT GAG CCC GTA ATA GCT TCC AAC TGG CAA AAG CTT GAA Gln Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu	383
115 120 125	
ACC TTC TGG CAC AAG CAT Thr Phe Trp His Lys His	401
130	

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met Ala	
1 5 10 15	

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu
 20 25 30

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys
 35 40 45

Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu Val
 50 55 60

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys
 65 70 75 80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
 85 90 95

Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln
 100 105 110

Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu Thr
 115 120 125

Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HD10-1-3

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC GTC ACA AAA TAC ATT ATG 47
 Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met
 1 5 10 15

GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTG TTG 95
 Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu
 20 25 30

CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGC 143

Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly
 35 40 45

TGC GTT GTA ATC GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA CTC
 Cys Val Val Ile Val Gly His Ile Glu Leu Gly Lys Pro Ala Leu
 50 55 60

GTT CCA GAC AAG GAG GTG TTG TAT CAA CAG TAC GAT GAG ATG GAG GAG
 Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu
 65 70 75

TGC TCG CAA GCC GCC CCA TAC ATC GAA CAA GCT CAG GTA ATA GCC CAC
 Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His
 80 85 90 95

CAG TTC AAG GAG AAA ATC CTT GGA CTG CTG CAG CGA GCC ACC CAA CAA
 Gln Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln
 100 105 110

CAA GCT GTC ATT GAG CCC GTA ATA GCT TCC AAC TGG CAA AAG CTT GAA
 Gln Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu
 115 120 125

ACC TTC TGG CAC AAG CAT
 Thr Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met Ala
 1 5 10 15

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu
 20 25 30

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys
 35 40 45

Val Val Ile Val Gly His Ile Glu Leu Gly Lys Pro Ala Leu Val
 50 55 60

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys
 65 70 75 80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
 85 90 95

Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln

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100

105

110

Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu Thr
 115 120 125

Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR36-20-164

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG	47
Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met	
1 5 10 15	

GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG	95
Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu	
20 25 30	

CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT	143
Leu Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly	
35 40 45	

TGT GTT GTG ATT GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC	191
Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile	
50 55 60	

GTT CCA GAC AAA GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG	239
Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu	
65 70 75	

TGC TCA CAA GCT GCC CCA TAT ATC GAA CAA GCT CAG GTA ATA GCT CAC	287
Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His	
80 85 90 95	

CAG TTC AAG GGA AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA	335
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125

Gln Phe Lys Gly Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln		
100	105	110
CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG		383
Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu		
115	120	125
GCC TTT TGG CAC AAG CAT		
Ala Phe Trp His Lys His		401
130		

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala			
1	5	10	15

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu			
20	25	30	

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys			
35	40	45	

Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val			
50	55	60	

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys			
65	70	75	80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln			
85	90	95	

Phe Lys Gly Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln			
100	105	110	

Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala			
115	120	125	

Phe Trp His Lys His
130

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala
1 5 10 15

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu
20 25 30

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys
35 40 45

Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val
50 55 60

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys
65 70 75 80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
85 90 95

Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln
100 105 110

Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala
115 120 125

Phe Trp His Lys His
130

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-20-165

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met 1 5 10 15	47
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu 20 25 30	95
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly 35 40 45	143
TGT GTT GTG ATT GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile 50 55 60	191
GTT CCA GAC AAA GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu 65 70 75	239
TGC TCA CAA GCT GCC CCA TAT ATC GAA CAA GCT CAG GTA ATA GCT CAC Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His 80 85 90 95	287
CAG TTC AAG GAA AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln 100 105 110	335
CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu 115 120 125	383
GCC TTT TGG CAC AAG CAT Ala Phe Trp His Lys His 130	401

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 1 5 10 15
Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu 20 25 30
Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys 35 40 45

Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val
 50 55 60

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys
 65 70 75 80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
 85 90 95

Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln
 100 105 110

Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala
 115 120 125

Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: PC-2-1
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 3..509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val	
20 25 30	
GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC	143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	
35 40 45	
GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	

50

55

60

CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC
 Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro
 65 70 75

239

GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG
 Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly
 80 85 90 95

287

TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC
 Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp
 100 105 110

335

CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG
 Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr
 115 120 125

383

TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC
 Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro
 130 135 140

431

ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG
 Ile Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu
 145 150 155

479

GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA
 Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu
 160 165

509

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly
 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala
 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60

Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly
 65 70 75 80

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp

85

90

95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110

Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile
 130 135 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160

Gly Val Asn Tyr Ala Thr Gly Asn Leu
 165

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-2-6

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	

AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val	
20 25 30	

GGC GGA GTT TAC TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC	143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	
35 40 45	

GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	
50 55 60	

CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro 65 70 75	239
GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly 80 85 90 95	287
TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp 100 105 110	335
CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr 115 120 125	383
TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro 130 135 140	431
ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG Ile Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu 145 150 155	479
GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu 160 165	509

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly 20 25 30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala 35 40 45
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro 50 55 60
Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly 65 70 75 80
Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile
 130 135 140
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160
 Gly Val Asn Tyr Ala Thr Gly Asn Leu
 165

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-4-1

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

A ACG TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC 46
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly
 1 5 10 15

GGC CCC ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC 94
 Gly Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val
 20 25 30

CTT GAG GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA CCC GGT TGC TCT 142
 Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser
 35 40 45

TTC TCT ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC 190
 Phe Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala
 50 55 60

TCT GCA GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT 238

Ser Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn			
65	70	75	
GAT TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA			286
Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu			
80	85	90	95
CAC GCA CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA			334
His Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg			
100	105	110	
TGC TGG GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA			382
Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala			
115	120	125	
GTC ACG GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT			430
Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala			
130	135	140	
GCC CTC TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC			478
Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe			
145	150	155	
TTG GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG			526
Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val			
160	165	170	175
CAG AAC TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG			574
Gln Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg			
180	185	190	
ATG GCA			580
Met Ala			

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly			
1	5	10	15

Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu		
20	25	30

Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe		
35	40	45

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser		
50	55	60

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His
 85 90 95

Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys
 100 105 110

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val
 115 120 125

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala
 130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
 165 170 175

Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 580 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-4-6

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 2..580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

A ACG TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly
 1 5 10 15

46

GGC CCC ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC

94

Gly Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val
 20 25 30

CTT GAG GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA CCC GGT TGC TCT
 Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser
 35 40 45

TTC TCT ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC
 Phe Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala
 50 55 60

TCT GCA GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT
 Ser Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn
 65 70 75

GAT TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA
 Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu
 80 85 90 95

CAC GCA CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA
 His Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg
 100 105 110

TGC TGG GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA
 Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala
 115 120 125

GTC ACG GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT
 Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala
 130 135 140

GCC CTC TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC
 Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe
 145 150 155

TTG GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG
 Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val
 160 165 170 175

CAG AAC TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG
 Gln Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg
 180 185 190

ATG GCA
 Met Ala

580

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear -

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

09899046 070601

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly
1 5 10 15

Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
20 25 30

Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
50 55 60

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His
85 90 95

Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys
100 105 110

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val
115 120 125

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala
130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
165 170 175

Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 959 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-3-4

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 3..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val	
20 25 30	
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	143
35 40 45	
GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	
50 55 60	
CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC	239
Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro	
65 70 75	
GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG	287
Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly	
80 85 90 95	
TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC	335
Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp	
100 105 110	
CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG	383
Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr	
115 120 125	
TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTC GGC GGC CCC	431
Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro	
130 135 140	
ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG	479
Ile Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu	
145 150 155	
GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA CCC GGT TGC TCT TTC TCT	527
Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser	
160 165 170 175	
ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC TCT GCA	575
Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala	
180 185 190	
GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT GAT TGC	623
Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys	
195 200 205	

CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA CAC GCA Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala 210 215 220	671
CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA TGC TGG Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp 225 230 235	719
GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA GTC ACG Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr 240 245 250 255	767
GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT GCC CTC Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu 260 265 270	815
TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC TTG GTA Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val 275 280 285	863
GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG CAG AAC Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn 290 295 300	911
TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG ATG GCA Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala 305 310 315	959

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly 20 25 30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala 35 40 45
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro 50 55 60
Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly 65 70 75 80
Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
100 105 110

Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile
130 135 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
145 150 155 160
Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
165 170 175

Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val
180 185 190

Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro
195 200 205

Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro
210 215 220

Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val
225 230 235 240

Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala
245 250 255

Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys
260 265 270

Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly
275 280 285

Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys
290 295 300

Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala
305 310 315

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 959 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-3-8

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 3..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr 1 5 10 15	47
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val 20 25 30	95
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg 35 40 45	143
GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln 50 55 60	191
CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro 65 70 75	239
Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly 80 85 90 95	287
TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp 100 105 110	335
CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr 115 120 125	383
TGC GGA TTC GCC GAT CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro 130 135 140	431
GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu 145 150 155	479
GAC GGG GTA AAC TAT CCA ACA GGG AAT TTA CCC GGT TGC TCT TTC TCT Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser 160 165 170 175	527
ATC TTT ATT CTT GCT CTT CTC TCG -TGT CTG ACC GTT CCG GCC TCT GCA Ile Phe Ile Leu Ala Leu Ser Cys Leu Thr Val Pro Ala Ser Ala 180 185 190	575
GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT GAT TGC	623

Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys		
195	200	205
CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA CAC GCA		671
Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala		
210	215	220
CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA TGC TGG		719
Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp		
225	230	235
GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA GTC ACG		767
Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr		
240	245	250
GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT GCC CTC		815
Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu		
260	265	270
TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC TTG GTA		863
Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val		
275	280	285
GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG CAG AAC		911
Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn		
290	295	300
TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG ATG GCA		959
Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala		
305	310	315

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn		
1	5	10
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly		
20	25	30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala		
35	40	45
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro		
50	55	60
Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly		
65	70	75
80		

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
100 105 110

Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Val
130 135 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
145 150 155 160

Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
165 170 175

Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val
180 185 190

Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro
195 200 205

Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro
210 215 220

Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val
225 230 235 240

Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala
245 250 255

Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys
260 265 270

Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly
275 280 285

Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys
290 295 300

Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala
305 310 315

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 959 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC C/E1

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53.:

CCATGAGCAC	GAATCCTAAA	CCTCAAAGAA	AAACCAAAAG	AAACACCAAC	CGTCGCCAC	60
AGGACGTCAA	GTTCCCGGGC	GGTGGTCAGA	TCGTTGGCGG	AGTTTACTTG	TTGCCCGCGCA	120
GGGGCCCTAG	GATGGGTGTG	CGCGCGACTC	GGAAGACTTC	GGAACGGTCG	CAACCCCGTG	180
GACGGCGTCA	GCCTATTCCC	AAGGCGCGCC	AGCCCACGGG	CCGGTCCTGG	GGTCAACCCG	240
GGTACCCATTG	GCCCCTTTAC	GCCAATGAGG	GCCTCGGGTG	GGCAGGGTGG	CTGCTCTCCC	300
CTCGAGGCTC	TCGGCCTAAT	TGGGGCCCCA	ATGACCCCCG	GCGAAAATCG	CGTAATTTGG	360
GTAAGGTCAT	CGATAACCCTA	ACGTGCGGAT	TCGCGATCT	CATGGGGTAY	ATCCCGCTCG	420
TAGGCGGCC	CRTTGGGGGC	GTGCGAAGGG	CTCTCGCACA	CGGTGTGAGG	GTCCTTGAGG	480
ACGGGGTAAA	CTATSCAACAA	GGGAATTAC	CCGGTTGCTC	TTTCTCTATC	TTTATTCTTG	540
CTCTTCTCTC	GTGTCTGACC	GTTCCGGCCT	CTGCAGTTCC	CTACCGAAAT	GCCTCTGGGA	600
TTTATCATGT	TACCAATGAT	TGCCCAAAC	CTTCCATAGT	CTATGAGGCA	GATAACCTGA	660
TCCTACACGC	ACCTGGTTGC	GTGCCTTGTG	TCATGACAGG	TAATGTGAGT	AGATGCTGGG	720
TCCAAATTAC	CCCTACACTG	TCAGCCCCGA	GCCTCGGAGC	AGTCACGGCT	CCTCTTCGGA	780
GAGCCGTTGA	CTACCTAGCG	GGAGGGGCTG	CCCTCTGCTC	CGCGTTATAC	GTAAGGAGACG	840
CGTGTGGGGC	ACTATTCTTG	GTAGGCCAAA	TGTTCACCTA	TAGGCCTCGC	CAGCACGCTA	900
CGGTGCAGAA	CTGCAACTGT	TCCATTACA	GTGGCCATGT	TACCGGCCAC	CGGATGGCA	959

(2) INFORMATION FOR SEQ ID NO: 54.:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54.:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5					10				15		

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly
 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala
 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60

Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly
 65 70 75 80

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110

Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Val
 130 135 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160

Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
 165 170 175

Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val
 180 185 190

Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro
 195 200 205

Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro
 210 215 220

Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val
 225 230 235 240

Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala
 245 250 255

Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys
 260 265 270

Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly
 275 280 285

Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys
 290 295 300

Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-1-37

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

ACCACCGGAG CTTCTATCAC ATACTCCACT TACGGCAAGT TCCTTGCTGA TGGAGGGTGT	60
TCAGGCGGCG CGCATGACGT GATCATATGC GACGAGTGCC ATTCCCAGGA CGCCACCACC	120
ATTCTTGGGA TAGGCAGTGT CCTTGACCAG GCAGAGACGG CTGGAGCTAG GCTCGTCGTC	180
TTGGCCACGG NCACCCCTCC CGGCAGTGTG ACAACGCCCG ACCCAAACAT CGAGGAAGTG	240
GCCCTGCCCTC AGGAGGGGGA GGTTCCCTTC TACGGCAGAG CCATTCCCCT TGCTTTATA	300
AAGGGTGGTA GGCATCTCAT CTTCTGCCAT TCCAAGAAAA ATTGTGATGA ACTC	354

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala			
1	5	10	15
10	15		

Asp Gly Gly Cys Ser Gly Gly Ala His Asp Val Ile Ile Cys Asp Glu			
20	25	30	
30			

Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr Val Leu
 35 40 45

Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Xaa
 50 55 60

Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu Glu Val
 65 70 75 80

Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala Ile Pro
 85 90 95

Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys
 100 105 110

Lys Asn Cys Asp Glu Leu
 115

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-1-48

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ACCACCGGAG CTTCTATCAC ATACTCCACT TACGGCAAGT TCCTTGCTGA TGGAGGGTGT	60
TCAGGCAGCG CGTATGACGT GATCATATGC GACGAGTGCC ATTCCCAGGA CGCCACCACC	120
ATTCTTGGGA TAGGCAGTGT CCTTGACCAAG GCAGAGACGG CTGGAGCTAG GCTCGTCGTC	180
TTGGNCACGG NCACCCCTCC CGGCAGTGTG ACAACGCCCG ACCCCAACAT CGAGGAAGTG	240
GCCCTGCCTC AGGAGGGGGA GGTTCCCTTC TACGGNAGAG CCATTCCCCT TGCTTTATA	300
AAGGGTGGTA GGCATCTCAT CTTCTGCCAT TCCAAGAAAA AATGTGATGA ACTT	354

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala
1 5 10 15

Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys Asp Glu
20 25 30

Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr Val Leu
35 40 45

Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Xaa Thr Xaa
50 55 60

Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu Glu Val
65 70 75 80

Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Xaa Arg Ala Ile Pro
85 90 95

Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys
100 105 110

Lys Lys Cys Asp Glu Leu Arg Gln Ala Thr Asp Gln Pro Gly Arg Glu
115 120 125

Arg Pro Trp Glu Tyr
130

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-1-37

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

ATGGCTTC	TGTCTCCGGA	CTTGGAGGTC	ATTACCA	NC	CTTGGGTTCT	GGTGGGGGGC	60
GTTGTGGCGA	CCCTGNCGNC	CTACTGCTTG	ACGGTGGGTT	CGGTAGCCAT	AGTCGGTAGG		120
ATCATCCTCT	CTGGGAAACC	TGCCATCATT	NCCGATA	AGGTATTATA	CCAGCAATT		180
GATGAGATGG	AGGAGTGCTC	GGCCTCGTTG	CCCTATATGG	ACGAAACACG	TNCCATTGCC		240
GGACAATTCA	AAGAGAAAGT	GCTCGGCTTC	AT	CCGACGA	CCGGCCAGAA	GGCTGAAACT	300
CTGAAGCCGG	CAGCCACGTC	TGTGTGGAAC	AAGGCTGATC	AGTTCTGGNC	CACATAC		357

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Met	Ala	Phe	Met	Ser	Pro	Asp	Leu	Glu	Val	Ile	Thr	Xaa	Thr	Trp	Val
1										10				15	
Leu	Val	Gly	Gly	Val	Val	Ala	Thr	Leu	Xaa	Xaa	Tyr	Cys	Leu	Thr	Val
													20	25	30
Gly	Ser	Val	Ala	Ile	Val	Gly	Arg	Ile	Ile	Leu	Ser	Gly	Lys	Pro	Ala
												35	40	45	
Ile	Ile	Xaa	Asp	Arg	Glu	Val	Leu	Tyr	Gln	Gln	Phe	Asp	Glu	Met	Glu
									50	55		60			
Glu	Cys	Ser	Ala	Ser	Leu	Pro	Tyr	Met	Asp	Glu	Thr	Arg	Xaa	Ile	Ala
									65	70		75		80	
Gly	Gln	Phe	Lys	Glu	Lys	Val	Leu	Gly	Phe	Ile	Ser	Thr	Thr	Gly	Gln
									85		90		95		
Lys	Ala	Glu	Thr	Leu	Lys	Pro	Ala	Ala	Thr	Ser	Val	Trp	Asn	Lys	Ala
									100		105		110		
Asp	Gln	Phe	Trp	Xaa	Thr	Tyr	Met	Trp	Asn	Phe	Ile	Ser	Gly	Ile	Gln
									115		120		125		

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-1-48

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

ATGGCTTGCA TGTCTGCGGA CCTGGAGGTC ATTACCANCA CTTGGGTTCT GGTGGGGGC	60
GTTGTGGCGN CCCTGGCGGC CTACTGCTTG ACGGTGGGTT CGGTAGCCAT AGTCGGTAGG	120
ATCATCCTCT CTGGGAAACC TGCCATCATT CCCGATAGGG AGGCATTATA CCANCAATT	180
GATGAGATGG AGGAGTGCTC GGCTCGTTG CCCTATATGG ACGAGACACG TGCCATTGCC	240
GGACAATTCA AAGAGAAAGT GCTCGGCTTC ATCAGCACGA CCGGCCAGAA GGCTGAAACT	300
CTGAAGCCGG CAGCCACGTC TGTGTGGAAC AAGGCTGANC AGTTCTGGC CACATAC	357

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Met Ala Cys Met Ser Ala Asp Leu Glu Val Ile Thr Xaa Thr Trp Val			
1	5	10	15

Leu Val Gly Gly Val Val Ala Xaa Leu Ala Ala Tyr Cys Leu Thr Val		
20	25	30

Gly Ser Val Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala		
35	40	45

Ile Ile Pro Asp Arg Glu Ala Leu Tyr Xaa Gln Phe Asp Glu Met Glu		
50	55	60

Glu Cys Ser Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala
65 70 75 80

Gly Gln Phe Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln
85 90 95

Lys Ala Glu Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala
100 105 110

Xaa Gln Phe Trp Ala Thr Tyr Met Trp Asn Phe Ile Ser Gly Ile Gln
115 120 125

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPri161"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ACCGGAGGCC AGGAGAGTGA TCTCCTCC

28

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPri162"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GGGCTGCTCT ATCCTCATCG ACGCCATC

28

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr163"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GCCAGAGGCT CGGAAGGCGA TCAGCGCT

28

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr164"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GAGCTGCTCT GTCTTCCTCG ACGCCGCA

28

(2) INFORMATION FOR SEQ ID NO: 67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr23"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

CTCATGGGGT ACATTCCGCT

20

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: YES
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr54"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

CTATTACCA TTCATCATCA TATCCA

27

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPr116"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

TTTTAAATAC ATCATGRCTG YATG

24

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPr66"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CTATTATTGT ATCCCRCTGA TGAARTTCCA CAT

33

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc_feature

- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr118:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ACTAGTCGAC TAYTGATCCR CTATRWARTT CCACAT

36

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr117:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

TTTTAAATAC ATCGCRCTGC ATGCA

25

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr119:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

ACTAGTCGAC TARTTGCATA GCCKRTTCAT CCAYTG

36

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr131:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

GGAATTCTAG ACCTCTGGGA YGARAYTGGA ARTG

34

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr130:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GGAATTCTAG ACGCTAYCAR GCACGTTGYG C

31

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..28
(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPr134:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CATATAGATG CCCACTTCCT ATC

23

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..28
(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPr3:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GTGTGCCAGG ACCATC

16

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr4:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

GACATGCATG TCATGATGTA

20

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr152:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TACGCCTCTT CTATATCGGT TGGGGCCTG

29

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr52:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

ATGTTGGGTA AGGTCATCGA TACCCCT

26

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr41:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CCCGGGAGGT CTCGTAGACC GTGCA

25

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr40:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CTATTAAAGA TAGAGAAAGA GCAACCGGG

29

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 192 to 203 of the V1 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 192 to 203 of the V1 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 213 to 223 of the V2 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Val Tyr Glu Ala Asp Asp Val Ile Leu His Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 213 to 233 of the V2 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 242 of the V3 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Val Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 242 of the V3 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Val Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 248 to 257 of the V4 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Val Arg Tyr Val Gly Ala Thr Thr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 248 to 257 of the V4 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Ala Pro Ser Leu Gly Ala Val Thr Ala Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 294 to 303 of the V5 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Arg Pro Arg Arg His Gln Thr Val Gln Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 294 to 303 of the V5 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Arg Pro Arg Gln His Ala Thr Val Gln Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 70 to 78 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Gln Pro Thr Gly Arg Ser Trp Gly Gln
1 5

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR33 and BR36

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 237 of the V3 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

Val Gln Asp Gly Asn Thr Ser Thr
1 5

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HD10

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 237 of the V3 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

Val Gln Asp Gly Asn Thr Ser Ala
1 5

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR36

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 248 to 257 of the V4 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

Val Lys Tyr Val Gly Ala Thr Thr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR36

(viii) POSITION IN GENOME:

(B) MAP POSITION: Positions 1688 to 1707 of HCV type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys Glu Val Leu Tyr Gln
1 5 10 15

Gln Tyr Asp Glu
20

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HD10

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1688 to 1707 of HCV type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

Leu Gly Gly Lys Pro Ala Leu Val Pro Asp Lys Glu Val Leu Tyr Gln
1 5 10 15

Gln Tyr Asp Glu
20

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1712 to 1731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
1 5 10 15

Phe Lys Glu Lys
20

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR36

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1724 to 1743 of HCV type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

Ile Ala His Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala
1 5 10 15

Thr Gln Gln Gln
20

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HD10

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1724 to 1743 of HCV type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

Ile Ala His Gln Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala
1 5 10 15

Thr Gln Gln Gln
20

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1688 to 1707 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Ala Leu Tyr Gln
1 5 10 15

Gln Phe Asp Glu
20

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1688 to 1707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val Leu Tyr Gln
1 5 10 15

Gln Phe Asp Glu
20

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: position 1712 to 1731 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

Ser Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln
1 5 10 15

Phe Lys Glu Lys
20

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1724 to 1743 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

Ile Ala Gly Gln Phe Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr
1 5 10 15

Gly Gln Lys Ala
20

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB48-3-10

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GTC TAT	46
Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAC CTG GAG CCC GAA GCC CGC AAG GCA ATT ACC GCC CTA	94
Gln Cys Cys Asp Leu Glu Pro Ala Arg Lys Ala Ile Thr Ala Leu	
20 25 30	
ACA GAG AGA CTC TAC GTG GGC GGT CCC ATG CAT AAC AGC AAG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp	
35 40 45	
CTG TGC GGG TAT CGC AGA TGT CGC GCA AGC GGC GTC TAC ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACA CTG ACG TGC TAC CTC AAA GCC TCA GCC GCT ATC AAA	238
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Lys	
65 70 75	
GCG GCG GGG CTG AGA GAC TGC ACC ATG TTG GTC TGT GGT GAT GAC CTG	286
Ala Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTT GTC ATC GCT GAG AGC GAT GGC GTA GAG GAG GAC AAA CGA CCC CTC	334
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Pro Leu	
100 105 110	
GGA GCC	340
Gly Ala	

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Val Tyr Gln	
1 5 10 15	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB215-3-8

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

C TCC ACT GTA ACC GAA AAA GAC ATC AGG GTC GAG GAG GAG GTA TAT	46
Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAC CTG GAG CCC GAA GCC CGC AAG GTA ATT ACC GCC CTA	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu	
20 25 30	
ACA GAG AGA CTC TAT GTG GGC GGT CCC ATG CAT AAT AGC AAA GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp	
35 40 45	
CTG TGC GGG TAT CGC AGA TGC CGC GCA AGC GGC GTC TAC ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACA CTG ACG TGC TAT CTC AAA GCC TCA GCC GCC ATC AGG	238
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg	
65 70 75	
GCG TCA GGG CTG AGA GAC TGC ACT ATG CTG GTC TAT GGT GAC GAC CTG	286
Ala Ser Gly Leu Arg Asp Cys Thr Met Leu Val Tyr Gly Asp Asp Leu	
80 85 90 95	
GTC GTC ATT GCC GAG AGC GAT GGC GTA GAG GAG GAC AAA CGA GCC CTC	334
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu	
100 105 110	
GGA GTC	340
Gly Val	

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
 1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr
 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
 50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
 65 70 75 80

Ser Gly Leu Arg Asp Cys Thr Met Leu Val Tyr Gly Asp Asp Leu Val
 85 90 95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
 100 105 110

Val

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB358-3-3

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GAG GTG TAT

Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
100 105 110

Ala

(2) INFORMATION FOR SEO ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE:

(B) CLONE: GB549-3-6

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

46

CAG TGC TGC GAC CTG GAG CCC GAA GCC CGC AAG GTG ATA TCC GCC CTA
 Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu
 20 25 30

94

ACG GAA AGA CTC TAC GTG GGC GGT CCC ATG TAC AAC TCC AAG GGG GAC
 Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp
 35 40 45

142

CTA TGC GGG CAA CGG AGG TGC CGC GCA AGC GGG GTC TAC ACC ACC AGC
 Leu Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser
 50 55 60

190

TTC GGG AAC ACT GTA ACG TGT TAT CTC AAG GCC GTT GCG GCT ACT AGG
 Phe Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg
 65 70 75

238

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GCC GCA GGT CTG AAA GGT TGC AGC ATG CTG GTT TGT GGA GAC GAC TTA
Ala Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu
     80          85          90          95

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286

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr					
1	5	10	15		
CAG TGT TGT GAC CTG GAG CCC GAG GCC CGC AAG GCA ATT ACT GCC CTA					94
Gln Cys Cys Asp Leu Glu Pro Ala Arg Lys Ala Ile Thr Ala Leu					
20		25		30	
ACA GAG AGA CTC TAT GTG GGC GGT CCC ATG CAT AAC AGC AAG GGA GAC					142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp					
35		40		45	
CTG TGT GGG TAT CGC AGA TGC CGC GCA AGC GGC GTC TAC ACC ACC AGC					190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Ser					
50		55		60	
TTC GGG AAC ACA CTG ACG TGC TAC CTC AAA GCC TCA GCC GCT ATC AGA					238
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg					
65		70		75	
GCG GCG GGG CTG AGA GAC TGC ACC ATG TTG GTC TGT GGT GAT GAC CTG					286
Ala Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu					
80		85		90	
				95	
GTC GTC ATC GCT GAG AGC GAT GGC GTT GAG GAG GAC AAA CGA GCC CTC					334
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu					
100		105		110	
GGA GCC					340
Gly Ala					

(2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln				
1	5	10	15	
Cys Cys Asp Leu Glu Pro Ala Arg Lys Ala Ile Thr Ala Leu Thr				
20		25		30
Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu				
35		40		45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Ser Phe				
50		55		60
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala				
65		70		80

GTC GTC ATC TGC GAG AGC GGC GGC GTA GAG GAG GAT GCA AGA GCC CTC	334	
Val Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu		
100	105	110
CGA GCC		340
Arg Ala		

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr Gln			
1	5	10	15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr			
20	25	30	

Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu			
35	40	45	

Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Ser Phe			
50	55	60	

Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg Ala			
65	70	75	80

Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val			
85	90	95	

Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg			
100	105	110	

Ala

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: GB809-3-1

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

C TCC ACT GTG ACT GAG AGA GAC ATC AAG GTC GAA GAA GAA GTC TAT	46
Ser Thr Val Thr Glu Arg Asp Ile Lys Val Glu Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAT CTG GAG CCC GAG GCC CGC AAG GTA ATA GCC GCC CTC	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ala Ala Leu	
20 25 30	
ACG GAG AGA CTC TAC GTG GGC GGC CCC ATG CAT AAC AGC AAG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp	
35 40 45	
CTT TGC GGG TAT CGT AGA TGC CGC GCG AGC GGC GTA TAC ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACA ATG ACG TGC TAC CTT AAG GCC TCA GCA GCC ATC AGG	238
Phe Gly Asn Thr Met Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg	
65 70 75	
GCT GCG GGG CTA AAG GAT TGC ACC ATG CTG GTT TGC GGT GAC GAC CTA	286
Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTC GTG ATC GCC GAG AGC GGT GGC GTT GAG GAG GAC AAA CGA GCC CTC	334
Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu	
100 105 110	
GGA GCT	340
Gly Ala	

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

Ser Thr Val Thr Glu Arg Asp Ile Lys Val Glu Glu Glu Val Tyr Gln	
1 5 10 15	

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ala Ala Leu Thr
 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
 50 55 60

Gly Asn Thr Met Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
 65 70 75 80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95

Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GB358-4-1

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC 48
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

CCT GTG GGT GGC GTC GCC AGG GCC CTG GCA CAC GGT GTT AGG GCT GTG 96
 Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
 20 25 30

GAG GAC GGG ATC AAT TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC 144
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45

180

TCT ATC TTC CTC TTG GCA CTT CTT TCG TGC CTG ACT GTT CCC ACC TCG Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	192
50 55 60	
GCC GTC AAC TAT CGC AAT GCC TCG GGC ATC TAT CAC ATC ACC AAT GAC Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp	240
65 70 75 80	
TGC CCG AAC TCG AGC ATA GTG TAC GAG ACC GAG CAC CAC ATC CTA CAC Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His	288
85 90 95	
CTC CCA GGG TGT TTA CCC TGC GTG AGG GTT GGG AAT CAG TCA CGC TGC Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys	336
100 105 110	
TGG GTG GCC CTC ACT CCC ACC GTG GCG GCG CCT TAC ATC GGC GCT CCG Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro	384
115 120 125	
CTT GAA TCC CTC CGG AGT CAT GTG GAT CTG ATG GTA GGT GCC GCT ACT Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr	432
130 135 140	
GCG TGC TCC GCT CTT TAC ATC GGA GAC CTG TGC GGT GGC GTA TTC TTG Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu	480
145 150 155 160	
GTT GGT CAG ATG TTC TCT TTC CAG CCG CGG CGC CAC TGG ACT ACG CAG Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln	528
165 170 175	
GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC GTT ACG GGC CAC AGG A Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg	574
180 185 190	

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
Ser Ile Phe Leu Leu Ala Leu Ser Cys Leu Thr Val Pro Thr Ser	

50

55

60

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His
 85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys
 100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro
 115 120 125

Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140

Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg
 180 185 190

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB549-4-3

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

ACG TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

48

CCT GTG GGT GGC GTC GCC AGG GCC TTG GCA CAT GGT GTC AGG GCC GTG
 Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
 20 25 30

96

GAG GAC GGG ATT AAC TAT GCA ACA GGG AAT CTT CCC GGT TGC TCC TTT Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45	144
TCT ATC TTC CTT CTA GCA CTT CTC TCG TGC TTG ACT GTC CCG GCC TCG Ser Ile Phe Leu Leu Ala Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60	192
GCG CAG CAC TAC CGG AAC ATC TCG GGC ATT TAT CAC GTC ACC AAT GAC Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80	240
TGC CCG AAC TCT AGT ATA GTG TAT GAA GCT GAC CAT CAT ATC ATG CAT Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His 85 90 95	288
CTA CCA GGG TGT GTG CCT TGC GTG AGA ACC GGG AAC ACC TCG CGC TGC Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys 100 105 110	336
TGG GTT CCT TTA ACA CCC ACT GTG GCT GCC CCC TAT GTT GGC GCG CCG Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro 115 120 125	384
CTC GAA TCC ATG CGG CGG CAC GTG GAC TTA ATG GTG GGT GCC ACC Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140	432
GTC TGC TCG GCC CTG TAC ATC GGA GAC CTT TGC GGA GGT GTC TTC CTG Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu 145 150 155 160	480
GTC GGG CAG ATG TTC ACC TTC CGG CCG CGC CGC CAT TGG ACT ACC CAG Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln 165 170 175	528
GAC TGC AAC TGC TCT ATC TAT GAT GGC CAC ATC ACC GGC CAT AGA A Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg 180 185 190	574

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30

183

Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe
35						40					45				
Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser
50						55					60				
Ala	Gln	His	Tyr	Arg	Asn	Ile	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp
65						70				75				80	
Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	His	His	Ile	Met	His
						85				90				95	
Leu	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Thr	Gly	Asn	Thr	Ser	Arg	Cys
						100			105				110		
Trp	Val	Pro	Leu	Thr	Pro	Thr	Val	Ala	Ala	Pro	Tyr	Val	Gly	Ala	Pro
						115			120			125			
Leu	Glu	Ser	Met	Arg	Arg	His	Val	Asp	Leu	Met	Val	Gly	Ala	Ala	Thr
						130			135			140			
Val	Cys	Ser	Ala	Leu	Tyr	Ile	Gly	Asp	Leu	Cys	Gly	Gly	Val	Phe	Leu
						145			150			155			160
Val	Gly	Gln	Met	Phe	Thr	Phe	Arg	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln
						165			170			175			
Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Asp	Gly	His	Ile	Thr	Gly	His	Arg	
						180			185			190			

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GB809-4-3

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

ACG TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala 1 5 10 15			
CCC GTT GGG GGC GTC GCC AGG GCC CTG GCG CAT GGC GTC AGG GCT GTG Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30			96
GAG GAC GGG ATT AAC TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45			144
TCT ATC TTC CTC CTG GCA CTT TCG TGC CTC ACT GTC CCA GCG TCA Ser Ile Phe Leu Leu Ala Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60			192
GCT GAG CAC TAC CGG AAT GCT TCG GGC ATC TAT CAC ATC ACC AAT GAC Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80			240
TGT CCG AAT TCC AGC GTA GTC TAT GAA ACT GAC CAC CAT ATA TTG CAC Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His 85 90 95			288
TTG CCG GGG TGC GTA CCC TGC GTG AGG GCC GGG AAC GTG TCT CGT TGC Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys 100 105 110			336
TGG ACG CCG GTA ACA CCT ACG GTG GCT GCC GTA TCC ATG GAC GCT CCG Trp Thr Pro Val Thr Pro Val Ala Ala Val Ser Met Asp Ala Pro 115 120 125			384
CTC GAG TCC TTC CGG CGG CAT GTG GAC CTA ATG GTA GGT GCG GCC ACC Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140			432
GTG TGT TCT GTC CTC TAT GTT GGA GAC CTC TGT GGA GGT GCT TTC CTA Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu 145 150 155 160			480
GTG GGG CAG ATG TTC ACC TTC CAG CCG CGT CGC CAC TGG ACC ACG CAG Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175			528
GAT TGT AAT TGC TCC ATC TAT ACT GGC CAT ATC ACC GGC CAC AGG A Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg 180 185 190			574

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

TGGGGATCCC GTATGATACC CGCTGCTTG A

31

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HcPr207"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

GGCGGAATTC CTGGTCATAG CCTCCGTGAA

30

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
50 55 60

Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
65 70 75 80

Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His
85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys
100 105 110

Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro
115 120 125

Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
130 135 140

Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu
145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg
180 185 190

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr206"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Amino acid
- (C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Amino acid
- (C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Val Tyr Glu Thr Glu His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Val Tyr Glu Ala Asp His His Ile Met His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Val Tyr Glu Thr Asp His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Val Arg Val Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

Val Arg Thr Gly Asn Thr Ser Arg Cys Trp Val Pro Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

Val Arg Ala Gly Asn Val Ser Arg Cys Trp Thr Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

Ala Pro Tyr Ile Gly Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

Ala Pro Tyr Val Gly Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Ala Val Ser Met Asp Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB358 and GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

Gln Pro Arg Arg His Trp Thr Thr Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

Arg Pro Arg Arg His Trp Thr Thr Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

Arg Pro Arg Arg His Trp Thr Thr Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TGGGATATGA TGATGAACTG GTC

23

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

CCAGGTACAA CGAACCAAT TGCC

24

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 957 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..957

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACT AAC Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	48
1 5 10 15	
CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGC CAG ATC GTT GGT Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly	96
20 25 30	
GGA GTA TAC TTG TTG CCG CGC AGG GGC CCC CGG TTG GGT GTG CGC GCG Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	144
35 40 45	
ACG AGG AAA ACT TCC GAG CGG TCC CAG CCA CGT GGG AGG CGC CAG CCC Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	192
50 55 60	
ATC CCC AAA GAT CGG CGC CCC ACT GGC AAG TCC TGG GGA AAA CCA GGA Ile Pro Lys Asp Arg Arg Pro Thr Gly Lys Ser Trp Gly Lys Pro Gly	240
65 70 75 80	
TAC CCT TGG CCC CTG TAC GGG AAT GAG GGC CTC GGC TGG GCA GGG TGG Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp	288
85 90 95	
CTC CTG TCC CCC CGA GGG TCT CGC CCG TCA TGG GGC CCA ACT GAC CCC Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro	336
100 105 110	
CGG CAC AGG TCA CGC AAC TTG GGT AAG GTC ATC GAT ACC CTT ACG TGT Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys	384
115 120 125	
GGC TTT GCC GAC CTC ATG GGG TAC ATC CCT GTC GTC GGC GCC CCA GTT Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val	432
130 135 140	
GGT GGT GTC GCC AGA GCT CTC GCG CAT GGC GTG AGA GTT CTG GAA GAC Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp	480
145 150 155 160	

GGG ATA AAC TAT GCA ACA GGG AAC TTG CCC GGT TGC TCC TTT TCT ATC Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile 165 170 175	528
TTC TTA TTG GCC CTG CTA TCT TGT ATC ACT GTG CCG GTC TCC GGC TTG Phe Leu Leu Ala Leu Ser Cys Ile Thr Val Pro Val Ser Gly Leu 180 185 190	576
CAG GTC AAG AAC ACC AGC AGC TCT TAC ATG GTA ACC AAT GAC TGC CAG Gln Val Lys Asn Thr Ser Ser Tyr Met Val Thr Asn Asp Cys Gln 195 200 205	624
AAC AGT AGC ATC GTC TGG CAG CTC AGG GAT GCT GTT CTT CAC GTC CCC Asn Ser Ser Ile Val Trp Gln Leu Arg Asp Ala Val Leu His Val Pro 210 215 220	672
GGG TGT GTC CCT TGT GAG GAG AAG GGC AAC ATA TCC CGC TGT TGG ATA Gly Cys Val Pro Cys Glu Glu Lys Gly Asn Ile Ser Arg Cys Trp Ile 225 230 235 240	720
CCG GTT TCG CCC AAT ATA GCT GTG AGC CAA CCT GGT GCG CTT ACC AAG Pro Val Ser Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Leu Thr Lys 245 250 255	768
GCG CTG CGG ACG CAT ATT GAT ACC ATC ATT GCA TCC GCT ACG TTT TGC Gly Leu Arg Thr His Ile Asp Thr Ile Ile Ala Ser Ala Thr Phe Cys 260 265 270	816
TCT GCC CTG TAC ATA GGA GAC CTG TGT GGC GCG GTG ATG TTG GCT TCT Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Ala Val Met Leu Ala Ser 275 280 285	864
CAA GTC TTC ATC ATC TCG CCC CAG CAT CAT AAG TTT GTC CAG GAC TGC Gln Val Phe Ile Ile Ser Pro Gln His His Lys Phe Val Gln Asp Cys 290 295 300	912
AAC TGT TCC ATA TAC CCA GGC CAC ATC ACT GGA CAT CGG ATG GCG Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala 305 310 315	957

(2) INFORMATION FOR SEQ ID NO: 144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15
--

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Asp Arg Arg Pro Thr Gly Lys Ser Trp Gly Lys Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
100 105 110

Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val
130 135 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
145 150 155 160

Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
165 170 175

Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Gly Leu
180 185 190

Gln Val Lys Asn Thr Ser Ser Tyr Met Val Thr Asn Asp Cys Gln
195 200 205

Asn Ser Ser Ile Val Trp Gln Leu Arg Asp Ala Val Leu His Val Pro
210 215 220

Gly Cys Val Pro Cys Glu Glu Lys Gly Asn Ile Ser Arg Cys Trp Ile
225 230 235 240

Pro Val Ser Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Leu Thr Lys
245 250 255

Gly Leu Arg Thr His Ile Asp Thr Ile Ile Ala Ser Ala Thr Phe Cys
260 265 270

Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Ala Val Met Leu Ala Ser
275 280 285

Gln Val Phe Ile Ile Ser Pro Gln His His Lys Phe Val Gln Asp Cys
290 295 300

Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala
305 310 315

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 2..337

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

C TCA ACG GTC ACG GAG AGG GAC ATC AGA ACT GAG GAG TCC ATA TAC	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr	
1 5 10 15	
CTT GCT TGC TCT TTA CCC GAG CAG GCA CGG ACT GCC ATA CAC TCA CTG	94
Leu Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu	
20 25 30	
ACT GAG AGG CTT TAC GTG GGA GGG CCC ATG CTA AAC AGC AAA GGG CAA	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Leu Asn Ser Lys Gly Gln	
35 40 45	
ACC TGC GGA TAC AGA CGC TGC CGC GCC AGC GGA GTG TTC ACC ACT AGC	190
Thr Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser	
50 55 60	
ATG GGA AAT ACC ATC ACG TGC TAC GTG AAG GCA CAA GCA GCC TGT AAG	238
Met Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Gln Ala Ala Cys Lys	
65 70 75	
GCT GCG GGC ATA ATT GCC CCC ACG ATG CTG GTG TGC GGC GAC GAT CTA	286
Ala Ala Gly Ile Ile Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTT GTC ATC TCA GAG AGT CAG GGG ACC GAG GAG GAC GAG CGG AAC CTA	334
Val Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu	
100 105 110	
CGA GCC	340
Arg Ala	

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Thr	Glu	Glu	Ser	Ile	Tyr	Leu
1				5					10					15	
Ala	Cys	Ser	Leu	Pro	Glu	Gln	Ala	Arg	Thr	Ala	Ile	His	Ser	Leu	Thr
			20					25				30			
Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	Leu	Asn	Ser	Lys	Gly	Gln	Thr
				35			40				45				
Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Phe	Thr	Thr	Ser	Met
					55					60					
Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Val	Lys	Ala	Gln	Ala	Ala	Cys	Lys	Ala
	65				70			75				80			
Ala	Gly	Ile	Ile	Ala	Pro	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val
				85			90				95				
Val	Ile	Ser	Glu	Ser	Gln	Gly	Thr	Glu	Glu	Asp	Glu	Arg	Asn	Leu	Arg
			100				105				110				

Ala

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..345

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

ATG AGC ACA CTT CCT AAA CCA CAA AGA AAA ACC AAA AGA AAC ACC AAC

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

Met	Ser	Thr	Leu	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5						10					15

Pro Gly His Arg Thr Leu Ser Ser Gln Ala Ala Val Arg Ser Leu Val

20				25							30				
----	--	--	--	----	--	--	--	--	--	--	----	--	--	--	--

Glu Phe Thr Cys Tyr His Ala Gly Ala Pro Ser Trp Val Cys Val Gln

35				40						45					
----	--	--	--	----	--	--	--	--	--	----	--	--	--	--	--

Cys Ala Arg Leu Pro Ser Gly Arg Asn Leu Ala Val Gly Ala Asn Pro

50				55						60					
----	--	--	--	----	--	--	--	--	--	----	--	--	--	--	--

Ser Pro Gly Arg Ala Glu Pro Arg Ala Gly Pro Gly Leu Ser Pro Gly

65				70						75					80
----	--	--	--	----	--	--	--	--	--	----	--	--	--	--	----

Thr Leu Gly Pro Tyr Met Gly Met Arg Ala Ala Gly Gly Gln Gly Gly

85

90

95

Ser Cys Pro Arg Ala Ala Leu Ala Arg Arg Gly Ala Gln Met Thr Pro
 100 105 110

Gly Ala Gly
 115

(2) INFORMATION FOR SEQ ID NO: 149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..280

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

G GCC TGT GAC CTC AAG GAC GAG GCT AGG AGG GTG ATA ACT TCA CTC
 Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu
 1 5 10 15

46

ACG GAG CGG CTT TAC TGT GGT CCT ATG TTC AAC AGC AAG GGA CAA
 Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln
 20 25 30

94

CAC TGC GGT TAC CGC CGC TGC CGT GCT AGT GGG GTG CTA CCC ACC AGC
 His Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser
 35 40 45

142

TTC GGG AAC ACA ATC ACC TGT TAC ATC AAA GCA AAG GCA GCT ACC AAA
 Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys
 50 55 60

190

GCT GCC GGA ATT AAA AAT CCA TCA TTC CTT GTC TGC GGA GAT GAC TTG
 Ala Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu
 65 70 75

238

GTC GTG ATT GCT GAG AGT GCA GGG ATC GAT GAG GAC AGA GCG
 Val Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Arg Ala
 80 85 90

280

(2) INFORMATION FOR SEQ ID NO: 150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids

(B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu Thr
 1 5 10 15
 Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln His
 20 25 30
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe
 35 40 45
 Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys Ala
 50 55 60
 Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu Val
 65 70 75 80
 Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Arg Ala
 85 90

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 499 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..499

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC AAC
 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15

48

CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT CAG ATC GTT GGC
 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly
 20 25 30

96

GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC GCG Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala 35 40 45	144
ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG CCT Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro 50 55 60	192
ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC GGG Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly 65 70 75 80	240
TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG TGG Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp 85 90 95	288
CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC CCC Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro 100 105 110	336
CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG TGC Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys 115 120 125	384
GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC ATT Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile 130 135 140	432
GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG GAC Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp 145 150 155 160	480
GGG GTA AAC TAT GCA ACA G Gly Val Asn Tyr Ala Thr 165	499

(2) INFORMATION FOR SEQ ID NO: 152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly 20 25 30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60

Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly
 65 70 75 80

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110

Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile
 130 135 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160

Gly Val Asn Tyr Ala Thr
 165

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

ACG TGC GGA TTC GCC GAT CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly	
1 5 10 15	

CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu	
20 25 30	

GAG GAC GGG GTA AAC TAT CCA ACA GGG AAT TTA CCC GGT TGC TCT TTC	144
---	-----

Glu Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe			
35	40	45	
TCT ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC TCT			192
Ser Ile Phe Ile Leu Ala Leu Ser Cys Leu Thr Val Pro Ala Ser			
50	55	60	
GCA GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT GAT			240
Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp			
65	70	75	80
TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA CAC			288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His			
85	90	95	
GCA CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA TGC			336
Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys			
100	105	110	
TGG GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA GTC			384
Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val			
115	120	125	
ACG GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT GCC			432
Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala			
130	135	140	
CTC TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC TTG			480
Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu			
145	150	155	160
GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG CAG			528
Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln			
165	170	175	
AAC TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG ATG			576
Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met			
180	185	190	
CGC			579
Ala			

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly			
1	5	10	15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
20 25 30

Glu Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
50 55 60

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His
85 90 95

Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys
100 105 110

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val
115 120 125

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala
130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
165 170 175

Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

ACG TGC GGA TTC GCC GAC CTC GTG GGG TAC ATC CCG CTC GTA GGC GGC Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly	48
1 5 10 15	
CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAT GGT GTG AGG GTT CTT Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu	96
20 25 30	
GAG GAC GGG GTG AAT TAT GCA ACA GGG AAT CTG CCT GGT TGC TCT TTC Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	144
35 40 45	
TCT ATC TTC ATT CTT GCA CTT CTC TCG TGC CTC ACT GTC CCG GCC TCT Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	192
50 55 60	
GCA GTT CCC TAC CGA AAT GCC TCT GGG ATC TAT CAT GTC ACC AAT GAT Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp	240
65 70 75 80	
TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT GAT CTG ATC CTA CAC Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His	288
85 90 95	
GCA CCT GGC TGC GTG CCT TGT GTC AGG AAA GAT AAT GTG AGT AGG TGC Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys	336
100 105 110	
TGG GTC CAA ATT ACC CCC ACG CTG TCA GCC CCG AGC TTC GGA GCA GTC Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val	384
115 120 125	
ACG GCT CCC CTT CGG AGA GCC GTT GAT TAC TTG GTG GGA GGG GCT GCC Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala	432
130 135 140	
CTC TGC TCC GCG TTA TAC GTT GGA GAC GCG TGT GGG GCA CTA TTT TTG Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu	480
145 150 155 160	
GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAT GCT ACG GTG CAG Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln	528
165 170 175	
GAC TGC AAC TGT TCC ATC TAC AGT GGC CAC GTC ACC GGC CAT CAG ATG Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met	576
180 185 190	
GCA	579
Ala	

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
 20 25 30

Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
 50 55 60

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His
 85 90 95

Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys
 100 105 110

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val
 115 120 125

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala
 130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..530

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 3..527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

CA CCT ACG ACA GCT CTG CTG GTG GCC CAG TTA CTG CGG ATT CCC CAA Pro Thr Thr Ala Leu Leu Val Ala Gln Leu Leu Arg Ile Pro Gln	47
1 5 10 15	
GTG GTC ATT GAC ATC ATC GCA GGG AGC CAC TGG GGG GTC TTG TTT GCC Val Val Ile Asp Ile Ile Ala Gly Ser His Trp Gly Val Leu Phe Ala	95
20 25 30	
GCC GCA TAC TAT GCA TCG GTG GCT AAC TGG ACC AAG GTC GTG CTG GTC Ala Ala Tyr Tyr Ala Ser Val Ala Asn Trp Thr Lys Val Val Leu Val	143
35 40 45	
TTG TTT CTG TTT GCA GGG GTT GAT GCT ACT ACC CAG ATT TCG GGC GGC Leu Phe Leu Phe Ala Gly Val Asp Ala Thr Thr Gln Ile Ser Gly Gly	191
50 55 60	
TCC AGC GCC CAA ACG ACG TAT GGC ATC GCC TCA TTT ATC ACC CGC GGC Ser Ser Ala Gln Thr Thr Tyr Gly Ile Ala Ser Phe Ile Thr Arg Gly	239
65 70 75	
GCG CAG CAG AAA CTG CAG CTC ATA AAT ACC AAC GGA AGC TGG CAC ATC Ala Gln Gln Lys Leu Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile	287
80 85 90 95	
AAC AGG ACC GCC CTT AAT TGT AAT GAC AGC CTC CAG ACT GGG TTC ATA Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Ile	335
100 105 110	
GCC GGC CTC TTC TAC TAC CAT AAG TTC AAC TCT TCT GGA TGC CCG GAT Ala Gly Leu Phe Tyr Tyr His Lys Phe Asn Ser Ser Gly Cys Pro Asp	383
115 120 125	
CGG ATG GCT AGC TGT AGG GCC CTT GCC ACT TTT GAC CAG GGC TGG GGA Arg Met Ala Ser Cys Arg Ala Leu Ala Thr Phe Asp Gln Gly Trp Gly	431
130 135 140	
ACT ATC AGC TAT GCC AAC ATA TCG GGT CCC AGT GAT GAC AAA CCA TAT Thr Ile Ser Tyr Ala Asn Ile Ser Gly Pro Ser Asp Asp Lys Pro Tyr	479
145 150 155	
TGC TGG CAC TAT CCC CCA CGG CCG TGC GGA GTG GTG CCA GCC CAA GAG	527

Cys Trp His Tyr Pro Pro Arg Pro Cys Gly Val Val Pro Ala Gln Glu
 160 165 170 175

GTC
 Val

530

(2) INFORMATION FOR SEQ ID NO: 158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 176 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

Pro Thr Thr Ala Leu Leu Val Ala Gln Leu Leu Arg Ile Pro Gln Val
 1 5 10 15

Val Ile Asp Ile Ile Ala Gly Ser His Trp Gly Val Leu Phe Ala Ala
 20 25 30

Ala Tyr Tyr Ala Ser Val Ala Asn Trp Thr Lys Val Val Leu Val Leu
 35 40 45

Phe Leu Phe Ala Gly Val Asp Ala Thr Thr Gln Ile Ser Gly Gly Ser
 50 55 60

Ser Ala Gln Thr Thr Tyr Gly Ile Ala Ser Phe Ile Thr Arg Gly Ala
 65 70 75 80

Gln Gln Lys Leu Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile Asn
 85 90 95

Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Ile Ala
 100 105 110

Gly Leu Phe Tyr Tyr His Lys Phe Asn Ser Ser Gly Cys Pro Asp Arg
 115 120 125

Met Ala Ser Cys Arg Ala Leu Ala Thr Phe Asp Gln Gly Trp Gly Thr
 130 135 140

Ile Ser Tyr Ala Asn Ile Ser Gly Pro Ser Asp Asp Lys Pro Tyr Cys
 145 150 155 160

Trp His Tyr Pro Pro Arg Pro Cys Gly Val Val Pro Ala Gln Glu Val
 165 170 175

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

C TCG ACC GTT ACC GAA CAT GAC ATA ATG ACC GAA GAG TCC ATT TAC Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu Ser Ile Tyr	46
1 5 10 15	
CAA TCA TGT GAC TTG CAG CCC GAG GCA CGC GCA GCA ATA CGG TCA CTC Gln Ser Cys Asp Leu Gln Pro Glu Ala Arg Ala Ala Ile Arg Ser Leu	94
20 25 30	
ACC CAA CGC CTC TAC TGT GGA GGC CCC ATG TAC AAC AGC AAG GGG CAA Thr Gln Arg Leu Tyr Cys Gly Pro Met Tyr Asn Ser Lys Gly Gln	142
35 40 45	
CAG TGT GGT TAT CGC AGA TGC CGC GCC AGC GGC GTT TTC ACC ACC AGT Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser	190
50 55 60	
ATG GGC AAC ACC ATG ACG TGC TAC ATC AAG GCT TTA GCC TCC TGT AGA Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg	238
65 70 75	
GCC GCA AGG CTC CGG GAC TGC ACG CTC CTG GTG TGT GGT GAC GAT CTT Ala Ala Arg Leu Arg Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu	286
80 85 90 95	
G TG GGC ATC TGC GAG AGC CAG GGG ACA CAC GAG GAT GAA GCA AGC CTG Val Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Ser Leu	334
100 105 110	
AGA GCC Arg Ala	340

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu Ser Ile Tyr Gln
1 5 10 15

Ser Cys Asp Leu Gln Pro Glu Ala Arg Ala Ala Ile Arg Ser Leu Thr
20 25 30

Gln Arg Leu Tyr Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met
50 55 60

Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg Ala
65 70 75 80

Ala Arg Leu Arg Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Ser Leu Arg
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

C TCA ACC GCC ACC GAA CAT GAC ATA TTG ACT GAA GAG TCC ATA TAC
Ser Thr Ala Thr Glu His Asp Ile Leu Thr Glu Glu Ser Ile Tyr

1	5	10	15
CAA TCA TGT GAC TCG CAG CCC GAC GCA CGC GCA GCA ATA CGG TCA CTC Gln Ser Cys Asp Ser Gln Pro Asp Ala Arg Ala Ala Ile Arg Ser Leu 20		25	30
94			
·ACC CAA CGC TTG TTC TGT GGA GGC CCC ATG TAT AAC AGC AAG GGG CAA Thr Gln Arg Leu Phe Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln 35	40	45	
142			
CAA TGT GGT TAT CGC AGA TGC CGC GCC AGC GGC GTC TTC ACC ACC AGT Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser 50	55	60	
190			
ATG GGC AAC ACC ATG ACG TGC TAC ATT AAG GCT TTA GCC TCC TGT AGA Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg 65	70	75	
238			
ACC GCT GGG CTC CGG GAC TAC ACG CTC CTG GTG TGT GGT GAC GAT CAT Thr Ala Gly Leu Arg Asp Tyr Thr Leu Leu Val Cys Gly Asp Asp His 80	85	90	95
286			
GTG GCC ATC TGC GAG AGC CAG GGG ACA CAC GAG GAT GAA GCG AAC CTG Val Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Asn Leu 100	105	110	
334			
AGA GCC Arg Ala			340

(2) INFORMATION FOR SEQ ID NO: 162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Ser Thr Ala Thr Glu His Asp Ile Leu Thr Glu Glu Ser Ile Tyr Gln 1	5	10	15
Ser Cys Asp Ser Gln Pro Asp Ala Arg Ala Ala Ile Arg Ser Leu Thr 20	25	30	
Gln Arg Leu Phe Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln 35	40	45	
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met 50	55	60	
Gly Asn Thr Met Thr Cys Tyr Ile-Lys Ala Leu Ala Ser Cys Arg Thr 65	70	75	80
Ala Gly Leu Arg Asp Tyr Thr Leu Leu Val Cys Gly Asp Asp His Val 85	90	95	

092699046 - 070601

Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Asn Leu Arg
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..499

(x) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

ATG AGC ACG AAT CCT AAA CTT CAA AGA AAA ACC AAA CGT AAC ACC AAC Met Ser Thr Asn Pro Lys Leu Gln Arg Lys Thr Lys Arg Asn Thr Asn	48
1 5 10 15	
CGC CGC CCC ATG GAC GTT AAG TTC CCG GGT GGC CAG ATC GTT GGC Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly	96
20 25 30	
GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG TTG GGT GTG CGC GCG Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	144
35 40 45	
ACT CGG AAG ACT TCG GAG CGG TCG CAA CCT CGT GGG AGG CGC CAA CCT Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	192
50 55 60	
ATC CCC AAG GCG CGC CGA TCC GAG GGC AGA TCC TGG GCG CAG CCC GGG Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly	240
65 70 75 80	
TAT CCT TGG CCC CTT TAC GGC AAT GAG GGC TGT GGG TGG GCA GGG TGG Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp	288
85 90 95	
CTC CTG TCC CCT CGC GGG TCT CGG CCG TCT TGG GGC CCT AAT GAT CCC	336

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro			
100	105	110	
CGG CGG AGG TCC CGC AAC CTG GGT AAG GTC ATC GAT ACC CTA ACA TGC			384
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys			
115	120	125	
GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTA GGC GCC CCC GTG			432
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val			
130	135	140	
GGT GGC GTC GCC AGA GCC CTG GCA CAC GGT GTT AGG GCT GTG GAA GAC			480
Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp			
145	150	155	160
GGG ATC AAC TAC GCA ACA G			499
Gly Ile Asn Tyr Ala Thr			
165			

(2) INFORMATION FOR SEQ ID NO: 164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Met Ser Thr Asn Pro Lys Leu Gln Arg Lys Thr Lys Arg Asn Thr Asn			
1	5	10	15
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly			
20	25	30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala			
35	40	45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro			
50	55	60	
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly			
65	70	75	80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp			
85	90	95	
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro			
100	105	110	
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys			
115	120 -	125	
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val			
130	135	140	

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp
 145 150 155 160

Gly Ile Asn Tyr Ala Thr
 165

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAACGTA ACACCAACCG CCGCCCTATG	60
GACGTTAAGT TCCCAGGCGG TGGTCAGATC GTTGGCGGAG TTTACTTGTT GCCGCGCAGG	120
GGCCCCAGGT TGGGTGTGCG CGCGACTCGG AAGACTTCGG AGCGGTCGCA ACCTCGTGGG	180
AGGCGCCAAC CTATCCCCAA GGCGCGCCGA ACCGAGGGCA GATCCTGGGC GCAGCCCGGG	240
TATCCTTGGC CCCTTTACGG CAATGAGGGC TGTGGGTGGG CAGGGTGGCT CCTGTCCCCT	300
CGCGGNTCTC GNCGTCTTG GGGCCCCAAT GATCCCCGN GGAGATCCCG CAACTTGGGT	360
AAGGTCATCG ATACCCTAAC ATGCGGCTTC GCCGACCTCA TGGGATACAT CCCGCTTGT	420
GGCGCCCCCG TGGGTGGCGT CGCCAGGGCC CTGGCACATG GTGTTAGGGC TGTGGAAGAC	480
GGGATCAATT ATGCAACAG	499

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn

1	5	10	15
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly			
20	25	30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala			
35	40	45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro			
50	55	60	
Ile Pro Lys Ala Arg Arg Thr Glu Gly Arg Ser Trp Ala Gln Pro Gly			
65	70	75	80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp			
85	90	95	
Leu Leu Ser Pro Arg Xaa Ser Arg Xaa Ser Trp Gly Pro Asn Asp Pro			
100	105	110	
Arg Xaa Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu			
115	120	125	

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

ACA TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTA GGC GCC	48		
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala			
1	5	10	15
CCC GTG GGT GGC GTC GCC AGG GCC-CTG GCA CAT GGT GTT AGG GCT GTG	96		
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val			
20	25	30	
GAA GAC GGG ATC AAT TAT GCA ACA GGG AAC CTT CCC GGT TGC TCC TTT	144		

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe			
35	40	45	
TCT ATC TTC CTC TTG GCG CTC CTC TCG TGC CTG ACT GTT CCC ACA TCG			192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser			
50	55	60	
GCC GTT AAC TAT CGC AAT GCT TCG GGC ATT TAT CAC ATC ACC AAT GAC			240
Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp			
65	70	75	80
TGC CCG AAT GCA AGC ATA GTG TAC GAG ACC GAA AAT CAC ATC TTA CAC			288
Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His			
85	90	95	
CTC CCA GGG TGC GTA CCC TGT GTG AGG ACT GGG AAC CAG TCG CGG TGT			336
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys			
100	105	110	
TGG GTG GCC CTC ACT CCC ACA GTA GCG TCG CCA TAC GCC GGT GCT CCG			384
Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro			
115	120	125	
CTT GAG CCC TTG CGG CGT CAT GTG GAC CTG ATG GTA GGT GCT GCC ACC			432
Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr			
130	135	140	
ATG TGT TCC GCC CTC TAC ATC GGC GAC TTG TGC GGT GGC TTA TTC TTG			480
Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu			
145	150	155	160
GTG GGC CAA ATG TTC ACC TTC CAA CCG CGA CGT CAC TGG ACC ACT CAG			528
Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln			
165	170	175	
GAC TGC AAT TGT TCC ATC TAC ACG GGC CAC ATT ACG GGT CAT CGG ATG			576
Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met			
180	185	190	
GCA			579
Ala			

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala			
1	5	10	15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser
50 55 60

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
65 70 75 80

Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His
85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys
100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro
115 120 125

Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
130 135 140

Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu
145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(vi) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

ACA TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCC GTG GGT GGC GTC GCC AGA GCC CTG GCA CAC GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAA GAC GGG ATC AAC TAC GCA ACA GGG AAT CTC CCC GGT TGC TCC TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTC TTG GCA CTT CTC TCG TGC CTC ACT GTT CCC GCG TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GGC GTT AAC TAT CGC AAT GCT TCG GGC GTT TAT CAC ATC ACC AAC GAC	240
Gly Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp	
65 70 75 80	
TGC CCG AAT GCG AGC ATA GTG TAC GAG ACC GAC AAT CAC ATC TTA CAC	288
Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Asp Asn His Ile Leu His	
85 90 95	
CTC CCA GGG TGC GTA CCC TGT GTG AAG ACC GGG AAC CAG TCG CGG TGT	336
Leu Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTG GCC CTC ACT CCC ACA GTG GCG TCG CCT TAC GTC GGT GCT CCG	384
Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Val Gly Ala Pro	
115 120 125	
CTC GAG CCC TTG CGG CGC CAT GTG GAC CTG ATG GTA GGT GCT GCC ACC	432
Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr	
130 135 140	
G TG TGC TCC GCC CTC TAC GTC GGC GAC CTG TGC GGT GGC TTA TTC TTG	480
Val Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Leu Phe Leu	
145 150 155 160	
GTA GGC CAA ATG TTC ACC TTC CAA CCG CGA CGC CAC TGG ACG ACC CAG	528
Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln	
165 170 175	
GAC TGT AAT TGT TCC ATC TAC GCA GGG CAT ATT ACG GGC CAT CGG ATG	576
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met	
180 185 190	
GCT	579
Ala	

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
50 55 60

Gly Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp
65 70 75 80

Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Asp Asn His Ile Leu His
85 90 95

Leu Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys
100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Val Gly Ala Pro
115 120 125

Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
130 135 140

Val Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu
145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 579 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

ACA TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTG GGC GCC Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	48
1 5 10 15	
CCT GTT GGT GGC GTC GCC AGA GCC CTT GCG CAC GGC GTC AGG GCT GTG Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	96
20 25 30	
GAA GAC GGG ATT AAC TAT GCA ACA GGG AAC CTT CCT GGT TGC TCC TTT Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	144
35 40 45	
TCT ATC TTC CTT CTG GCA CTT CTC TCG TGC CTG ACT GTC CCC GCC TCG Ser Ile Phe Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	192
50 55 60	
GCT GTG CAT TAT CAC AAC ACC TCG GGC ATC TAC CAC CTC ACC AAT GAC Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Leu Thr Asn Asp	240
65 70 75 80	
TGC CCT AAC TCT AGC ATA GTC TTT GAG GCA GTC CAT CAC ATC TTG CAC Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Val His His Ile Leu His	288
85 90 95	
CTT CCA GGA TGC GTC CCT TGT GTA AGA ACT GGG AAC CAG TCT CGG TGC Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys	336
100 105 110	
TGG GTA GCC TTG ACC CCC ACG CTG GCC GCG CCA TAC CTT GGC GCT CCA Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro Tyr Leu Gly Ala Pro	384
115 120 125	
CTC GAG TCC ATG CGG CGT CAC GTG GAT TTG ATG GTG GGC ACT GCT ACA Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr	432
130 135 140	
TTG TGC TCA GCA CTC TAC GTT GGG GAC CTG TGC GGG GGC ATA TTC CTA Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ile Phe Leu	480
145 150 155 160	
GCG GGC CAG ATG TTC ACC TTC CGG CCC CGC CTC CAT TGG ACC ACC CAG Ala Gly Gln Met Phe Thr Phe Arg Pro Arg Leu His Trp Thr Thr Gln	528
165 170 175	

GAG TGC AAT TGT TCC ACC TAT CCG GGC CAC ATC ACG GGT CAT AGA ATG
 Glu Cys Asn Cys Ser Thr Tyr Pro Gly His Ile Thr Gly His Arg Met
 180 185 190

576

GCG
 Ala

579

(2) INFORMATION FOR SEQ ID NO: 172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
 50 55 60

Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Leu Thr Asn Asp
 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Val His His Ile Leu His
 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys
 100 105 110

Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro Tyr Leu Gly Ala Pro
 115 120 125

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr
 130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ile Phe Leu
 145 150 155 160

Ala Gly Gln Met Phe Thr Phe Arg Pro Arg Leu His Trp Thr Thr Gln
 165 170 175

Glu Cys Asn Cys Ser Thr Tyr Pro Gly His Ile Thr Gly His Arg Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

ACG TGC GGT TCC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC Thr Cys Gly Ser Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	48
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC TTG GCG CAT GGC GTC AGG GCT GTG Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	96
20 25 30	
GAG GAC GGG ATA AAC TAT GCA ACA GGG AAC CTT CCT GGT TGC TCT TTT Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	144
35 40 45	
TCT ATC TTC CTT CTG GCA CTT CTC TCG TGC CTG ACT GTC CCC GCC TCA Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	192
50 55 60	
GCT GTG CAT TAT CAC ACC TCG GGC ATC TAT CAC ATC ACT AAT GAC Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Ile Thr Asn Asp	240
65 70 75 80	
TGC CCT AAC TCT AGC ATA GTC TTT GAG GCA GAG CAT CAC ATC TTG CAT Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Glu His His Ile Leu His	288
85 90 95	
CTT CCA GGA TGC GTC CCC TGT GTG AGA ACT GGG AAC CAG TCA CGA TGC Leu Pro Gly Cys Val Pro Cys Val-Arg Thr Gly Asn Gln Ser Arg Cys	336
100 105 110	
TGG ATA GCC TTG ACC CCT ACG TTG GCC GCG CCA CAC ATT GGC GCT CCA Trp Ile Ala Leu Thr Pro Thr Leu Ala Ala Pro His Ile Gly Ala Pro	384

115

120

125

CTT GAG TCC ATG CGA CGT CAT GTG GAT TTG ATG GTA GGC ACT GCC ACA Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr 130	135	140	432	
TTG TGC TCC GCA CTC TAC ATT GGA GAT CTG TGC GGA GGC ATA TTT CTA Leu Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ile Phe Leu 145	150	155	160	480
GTG GGC CAG ATG TTC AAC TTC AGG CCC CGC CTG CAC TGG ACC ACC CAG Val Gly Gln Met Phe Asn Phe Arg Pro Arg Leu His Trp Thr Thr Gln 165	170	175	528	
GAG TGC AAT TGT TCC ATC TAT CCA GGC CAC ATC ACG GGT CAC AGA ATG Glu Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met 180	185	190	576	
GCG Ala			579	

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

Thr Cys Gly Ser Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala 1	5	10	15
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20	25	30	
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35	40	45	
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50	55	60	
Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Ile Thr Asn Asp 65	70	75	80
Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Glu His His Ile Leu His 85	90	95	
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys 100	105	110	
Trp Ile Ala Leu Thr Pro Thr Leu Ala Ala Pro His Ile Gly Ala Pro 115	120	125	

224

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr
 130 135 140

Leu Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ile Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Asn Phe Arg Pro Arg Leu His Trp Thr Thr Gln
 165 170 175

Glu Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

ACG TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	

CCT GTG GGT GGC GTC GCC AGG GCC TTG GCA CAT GGT GTC AGG GCC GTG	96
Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	

GAG GAC GGG ATT AAC TAT GCA ACA GGG AAT CTT CCC GGT TGC TCC TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	

TCT ATC TTC CTT CTA GCA CTT CTC TCG TGC TTG ACT GTC CCG GCC TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu-Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	

GCG CAG CAC TAC CGG AAC ATC TCG GGC ATT TAT CAC GTC ACC AAT GAC	240
Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp	

225

65

70

75

80

TGC CCG AAC TCT AGT ATA GTG TAT GAA GCT GAC CAT CAT ATC ATG CAT
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His
 85 90 95

288

CTA CCA GGG TGT GTG CCT TGC GTG AGA ACC GGG AAC ACC TCG CGC TGC
 Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys
 100 105 110

336

TGG GTT CCT TTA ACA CCC ACT GTG GCT GCC CCC TAT GTT GGC GCG CCG
 Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro
 115 120 125

384

CTC GAA TCC ATG CGG CGG CAC GTG GAC TTA ATG GTG GGT GCC GCC ACC
 Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140

432

GTC TGC TCG GCC CTG TAC ATC GGA GAC CTT TGC GGA GGT GTC TTC CTG
 Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
 145 150 155 160

480

GTC GGG CAG ATG TTC ACC TTC CCG CCG CGC CAT TGG ACT ACC CAG
 Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln
 165 170 175

528

GAC TGC AAC TGC TCT ATC TAT GAT GGC CAC ATC ACC GGC CAT AGA ATG
 Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg Met
 180 185 190

576

GCT
 Ala

579

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
 50 55 60

Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp
 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His
 85 90 95
 Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys
 100 105 110

Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro
 115 120 125

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

ACG TGC GGG TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCT
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

48

CCA GTA GGA GGC GTC GCC AGA GCC TTG GCG CAT GGC GTC AGG GCT GTG
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val

96

227

20

25

30

GAG GAC GGG ATC AAT TAC GCA ACA GGG AAC CTT CCC GGC TGC TCC TTT Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35	40	45	144
TCT ATC TTC CTC TTG GTA CTT CTC TCG CGC CTA ACT GTC CCA GCG TCT Ser Ile Phe Leu Leu Val Leu Leu Ser Arg Leu Thr Val Pro Ala Ser 50	55	60	192
GCT CAG CAC TAC CGG AAT GCA TCG GGC ATC TAC CAT GTC ACC AAC GAC Ala Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp 65	70	75	240
TGC CCG AAC TCC AGT ATT GTG TAT GAA GCC GAC CAT CAC ATC ATG CAC Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His 85	90	95	288
CTA CCC GGG TGT GTG CCC TGT GTA AGA ACT GGG AAT GTC TCG CGT TGC Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys 100	105	110	336
TGG ATT CCT TTA ACA CCC ACT GTA GCC GTC CCC TAC CTC GGG GCT CCA Trp Ile Pro Leu Thr Pro Thr Val Ala Val Pro Tyr Leu Gly Ala Pro 115	120	125	384
CTT ACG TCT GTA CGG CAG CAT GTG GAC CTG ATG GTG GGG GCG GCC ACC Leu Thr Ser Val Arg Gln His Val Asp Leu Met Val Gly Ala Ala Thr 130	135	140	432
TTA TGC TCT GCC CTC TAC ATC GGA GAC CAT TGC GGA GGT GTC TTC TTG Leu Cys Ser Ala Leu Tyr Ile Gly Asp His Cys Gly Val Phe Leu 145	150	155	480
GCA GGG CAG ATG GTC AGT TTC CAA CCC CGG CGT CAT TGG ACT ACC CAG Ala Gly Gln Met Val Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165	170	175	528
GAT TGC AAC TGT TCC ATC TAT GTG GGC CAC ATC ACC GGC CAC AGG ATG Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met 180	185	190	576
GCC Ala			579

(2) INFORMATION FOR SEQ ID NO: 178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45

Ser Ile Phe Leu Leu Val Leu Leu Ser Arg Leu Thr Val Pro Ala Ser
 50 55 60

Ala Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His
 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys
 100 105 110

Trp Ile Pro Leu Thr Pro Thr Val Ala Val Pro Tyr Leu Gly Ala Pro
 115 120 125

Leu Thr Ser Val Arg Gln His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140

Leu Cys Ser Ala Leu Tyr Ile Gly Asp His Cys Gly Gly Val Phe Leu
 145 150 155 160

Ala Gly Gln Met Val Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

ACCTGCGGCT TCGCCGACCT CATGGGATAC ATCCCCTCG TAGGCAGCCC CGTGGGAGGC	60
GTCGCCAGAR CTCTGGCGCA TGGCGTCAGG GCTCTGGAAG ACGGGATCAA TTATGCAACA	120
GGGAATCTTC CTGGTTGCTC TTTCTCTATC TCCCTTCTTG AACTTCTCTC GTGCCTGACT	180
GTTCCCGCCT CAGCCATCCA CTATCGCAAT GCTTCGGACG GTTATTATAT CACCAATGAT	240
TGCCCCGAACT CTAGCATAGT GTATGAAGCC GAGAACACCA TCTTGCACCT TCCGGGGTGT	300
ATACCCCTGTG TGAAGACCGG GAATCAGTCG CGGTGCTGGG TGGCTCTCAC CCCCACGCTG	360
GCGGCCAC ACCTACGTGC TCCGCTTTCG TCCTTACGGG CGCATGTGGA CCTAATGGTG	420
GGGGCCGCCA CGGCATGCTC CGCTTTTAC ATTGGAGATC TGTGCGGGGG TGTGTTTTG	480
GCGGGCCAAC TGTTCACTAT CCGGCCACGC ATTCAATGAAA CCACTCAGGA CTGCAATTGC	540
TCCATCTACT CAGGGCACAT CACGGTNNN NNNNNNNNN	579

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala			
1	5	10	15

Pro Val Gly Gly Val Ala Arg Xaa Leu Ala His Gly Val Arg Ala Leu		
20	25	30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe		
35	40	45

Ser Ile Ser Leu Leu Glu Leu Ser Cys Leu Thr Val Pro Ala Ser		
50	55	60

Ala Ile His Tyr Arg Asn Ala Ser Asp Gly Tyr Tyr Ile Thr Asn Asp			
65	70	75	80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Glu Asn His Ile Leu His		
85	90	95

Leu Pro Gly Cys Ile Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys		
100	105	110

Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro His Leu Arg Ala Pro
 115 120 125

Leu Ser Ser Leu Arg Ala His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140

Ala Cys Ser Ala Phe Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
 145 150 155 160

Ala Gly Gln Leu Phe Thr Ile Arg Pro Arg Ile His Glu Thr Thr Gln
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Ile Thr Gly Xaa Xaa Xaa
 180 185 190

Xaa

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

GCCTGCGGCT TCGCCGATCT CATGGGATAC ATCCCGCTCG TAGGCCGCCC CGTGGGTGGC	60
GTCGCCAGAG CCCTGGCGCA CGGTGTTAGG GCTGTGGAGG ACGGGATTAA CTACGCAACA	120
GGGAATCTTC CTGGTTGCTC TTTCTCTATC TNCCCTCTGG CACTTCTCTC GTGCCTGACT	180
GTCCCCGGCCT CGGCTCAGCA CTACCGGAAT GTCTCGGGCA TCTACCACGT CACCAATGAT	240
TGCCCCGAATT CCAGCATAGT GTATGAAGCC GATCACCCACA TCATGCACTT ACCAGGGTGC	300
ATACCCCTGCG TGAGGGACCGG GAACGTTTCG CGCTGCTGGG TATCTCTGAC ACCTACTGTG	360
GCTGCTCCCT ACCTCGGGGC TCCGCTTACG TCGCTACGGC GGCATGTGGA TTTGATGGTG	420
GGTGCAGCCA CCCTTGCTC TGCCCTCTAC GTCGGAGACC TCTGTGGAGG TGTCTTCCTA	480

GTGGGACAGA TGTCACCTT CCAGCCGC CGCCACTGGA CCACTCAGGA CTGCAACTGC 540
TCCATTTACG TCGGCCACAT CACAGGCCAC AGAATGGCT 579

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Ala Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Xaa Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
50 55 60

Ala Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp
65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His
85 90 95

Leu Pro Gly Cys Ile Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys
100 105 110

Trp Val Ser Leu Thr Pro Thr Val Ala Ala Pro Tyr Leu Gly Ala Pro
115 120 125

Leu Thr Ser Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Val Phe Leu
145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

ACC TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	48
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC CTA GAA CAC GGT GTT AGG GCT GTG Pro Val Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val	96
20 25 30	
GAG GAC GGT ATT AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTT Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	144
35 40 45	
TCT ATC TCC CTC TTG GCA CTT CTT TCG TGC CTG ACT GTT CCC ACC TCA Ser Ile Ser Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	192
50 55 60	
GCC GTC AAC TAT CGC AAC GCC TCG GGC GTC TAT CAT ATC ACC AAT GAC Ala Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp	240
65 70 75 80	
TGC CCG AAT TCG AGC ATA GTG TAC GAG GCT GAC TAC CAC ATC CTA CAC Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Tyr His Ile Leu His	288
85 90 95	
CTC CCT GGG TGC TTA CCC TGC GTG AGG GTT GGG AAT CAG TCA CGC TGC Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys	336
100 105 110	
TGG GTG GCC CTT ACT CCC ACC GTG GCG GCG CCT TAC GTT GGT GCT CCG Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro	384

115

120

125

CTA GAA TCC CTC CGG AGT CAT GTG GAT CTG ATG GTA GGT GCT GCT ACT Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr 130	135	140	432	
GTG TGC TCC GCT CTT TAC ATC GGG GAC CTG TGC GGT GGC GTA TTT TTG Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu 145	150	155	160	480
GTT GGT CAG ATG TTT TCT TTC CAG CCG CGA CGC CAC TGG ACC ACG CAG Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165	170	175	528	
GAC TGC AAT TGT TCT ATC TAC GCG GGG CAC GTT ACG GGC CAC AGG ATG Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met 180	185	190	576	
GCA			579	
Ala				

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala 1	5	10	15
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20	25	30	
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35	40	45	
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser 50	55	60	
Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp 65	70	75	80
Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His 85	90	95	
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys 100	105	110	
Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro 115	120	125	
Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130	135	140	

Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Ala Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45

Ser Ile Ser Phe Trp His Phe Ser Arg Ala * Leu Ser Arg Pro Arg
 50 55 60

Leu Ser Thr Thr Gly Met Ser Arg Ala Ser Thr Thr Ser Pro Met Ile
 65 70 75 80

Ala Arg Ile Pro Ala * Cys Met Lys Pro Ile Thr Thr Ser Cys Thr
 85 90 95

Tyr Gln Gly Ala Tyr Pro Ala * Gly Pro Gly Thr Phe Arg Ala Ala
 100 105 110

Gly Tyr Leu * His Leu Leu Trp Leu Leu Pro Thr Ser Gly Leu Arg
 115 120 125

Leu Arg Arg Tyr Gly Gly Met Trp Ile * Trp Trp Val Gln Pro Pro
 130 135 140

Phe Ala Leu Pro Ser Thr Ser Glu Thr Ser Val Glu Val Ser Ser *
 145 150 155 160

Trp Asp Arg Cys Ser Pro Ser Ser Arg Ala Ala Thr Gly Pro Leu Arg
 165 170 175

Thr Ala Thr Ala Pro Phe Thr Ser Ala Thr Ser Gln Ala Thr Glu Trp

180

185

190

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala 1 5 10 15	48
CCC GTG GGT GGC GTC GCC AGA GCC CTG GAA CAT GGT GTT AGG GCT GTG Pro Val Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val 20 25 30	96
GAG GAC GGC ATC AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTC Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45	144
TCT ATC TAC CTC TTG GCA CTT CTC TCG TGC CTG ACT GTT CCC ACC TCG Ser Ile Tyr Leu Leu Ala Leu Ser Cys Leu Thr Val Pro Thr Ser 50 55 60	192
GCC ATC CAC TAT CGC AAT GCC TCG GGC GTC TAC CAC GTC ACC AAT GAC Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp 65 70 75 80	240
TGC CCG AAC TCG AGC ATA GTG TAC GAG GCC GAC CAC CAC ATC CTA CAC Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His 85 90 95	288
CTT CCA GGG TGC TTA CCC TGT GTG AGG GTT GGG AAT CAG TCA CGT TGT Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys 100 105 110	336
TGG GTG GCC CTC TCT CCC ACC GTG GCG GCG CCT TAC ATC GGT GCT CCA	384

Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro				
115	120	125		
GTT GAA TCC TTC CGG AGA CAC GTG GAC ATG ATG GTG GGC GCT GCT ACT				432
Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr				
130	135	140		
GTG TGC TCC GCT CTC TAT ATT GGG GAC TTG TGT GGT GGC GTA TTC TTG				480
Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu				
145	150	155	160	
GTT GGT CAG ATG TTT TCT TTC CGG CCA CGA CGC CAC TGG ACT ACG CAG				528
Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln				
165	170	175		
GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC ATC ACT GGC CAC GGA ATG				576
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met				
180	185	190		
GCA				579
Ala				

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala			
1	5	10	15

Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val			
20	25	30	

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe			
35	40	45	

Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser			
50	55	60	
Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp			
65	70	75	80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His			
85	90	95	

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys			
100	-105	110	

Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro			
115	120	125	

Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr
 130 135 140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(x) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	

CCT GTG GGT GGC GTC GCC AGG GCC CTG GCA CAC GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	

GAG GAC GGG ATC AAT TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	

TCT ATC TTC CTC TTG GCA CTT CTT TCG TGC CTG ACT GTT CCC ACC TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	
50 55 60	

GCC GTC AAC TAT CGC AAT GCC TCG GGC ATC TAT CAC ATC ACC AAT GAC	240
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Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
 65 70 75 80

TGC CCG AAC TCG AGC ATA GTG TAC GAG ACC GAG CAC CAC ATC CTA CAC
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His
 85 90 95

CTC CCA GGG TGT TTA CCC TGC GTG AGG GTT GGG AAT CAG TCA CGC TGC
 Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys
 100 105 110

TGG GTG GCC CTC ACT CCC ACC GTG GCG GCG CCT TAC ATC GGC GCT CCG
 Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro
 115 120 125

CTT GAA TCC CTC CGG AGT CAT GTG GAT CTG ATG GTA GGT GCC GCT ACT
 Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140

GCG TGC TCC GCT CTT TAC ATC GGA GAC CTG TGC GGT GGC GTA TTT TTG
 Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
 145 150 155 160

GTT GGT CAG ATG TTC TCT TTC CAG CCG CGG CGC CAC TGG ACT ACG CAG
 Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln
 165 170 175

GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC GTT ACG GGC CAC AGG ATG
 Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met
 180 185 190

GCA
 Ala 579

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45

Ser Ile Phe Leu Leu Ala Leu Ser Cys Leu Thr Val Pro Thr Ser
 50 55 60

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His
 85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys
 100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro
 115 120 125

Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140

Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(x) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

ACG TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

48

CCC GTT GGG GGC GTC GCC AGG GCC CTG GCG CAT GGC GTC AGG GCT GTG Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30	96
GAG GAC GGG ATT AAC TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45	144
TCT ATC TTC CTC CTG GCA CTT CTT TCG TGC CTC ACT GTC CCA GCG TCA Ser Ile Phe Leu Leu Ala Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60	192
GCT GAG CAC TAC CGG AAT GCT TCG GGC ATC TAT CAC ATC ACC AAT GAC Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80	240
TGT CCG AAT TCC AGC GTA GTC TAT GAA ACT GAC CAC CAT ATA TTG CAC Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His 85 90 95	288
TTG CCG GGG TGC GTA CCC TGC GTG AGG GCC GGG AAC GTG TCT CGT TGC Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys 100 105 110	336
TGG ACG CCG GTA ACA CCT ACG GTG GCT GCC GTA TCC ATG GAC GCT CCG Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro 115 120 125	384
CTC GAG TCC TTC CGG CGG CAT GTG GAC CTA ATG GTA GGT GCG GCC ACC Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140	432
GTG TGT TCT GTC CTC TAT GTT GGA GAC CTC TGT GGA GGT GCT TTC CTA Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu 145 150 155 160	480
GTG GGG CAG ATG TTC ACC TTC CAG CCG CGT CGC CAC TGG ACC ACG CAG Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175	528
GAT TGT AAT TGC TCC ATC TAT ACT GGC CAT ATC ACC GGC CAC AGG ATG Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met 180 185 190	576
CGC Ala	579

(2) INFORMATION FOR SEQ ID NO: 190:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
 50 55 60

Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
 65 70 75 80

Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His
 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys
 100 105 110

Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro
 115 120 125

Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140

Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS

00000000000000000000000000000000

(B) LOCATION: 1..289

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	48
1 5 10 15	
CGC CGC CCC ATG GAC GTT AAG TTC CCG GGC GGT GGC CAG ATC GTT GGT Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly	96
20 25 30	
GGA GTT TAC TTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	144
35 40 45	
ACT AGG AAG ACT TCG GAG CGG TCG CAA CCT CGT GGG AGA CGT CAG CCT Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	192
50 55 60	
ATC CCC AAG GCA CGT CGA TCT GAG GGA AGG TCC TGG GCT CAG CCC GGG Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly	240
65 70 75 80	
TAC CCA TGG CCT CTT TAC GGT AAT GAG GGT TGT GGG TGG GCA GGA TGG G Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp	289
85 90 95	

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly	
20 25 30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly	

65	70	75	80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp			
85	90	95	

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..498

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	48
1 5 10 15	
CGC CGC CCT ATG GAC GTA AAG TTC CCG GGC GGT GGA CAG ATC GTT GGC Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly	96
20 25 30	
GGA GTT TAC TTG TTG CCG CGC AGG GGC CCC CGG TTG GGT GTG CGC GCG Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	144
35 40 45	
ACT CGG AAG ACT TCG GAG CGG TCG CAA CCT CGT GGC AGG CGT CAA CCT Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	192
50 55 60	
ATC CCC AAG GCG CGC CGG TCC GAG GGC AGG TCC TGG GCG CAA GCC GGG Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Ala Gly	240
65 70 75 80	
TAC CCC TGG CCC CTC TAT GGC AAT GAG GGC TGT GGG TGG GCA GGG TGG Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp	288
85 90 95	
CTC CTG TCT CCT CGC GGC TCT CGG CCA TCT TGG GGC CCA AAT GAT CCC	336

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro		
100	105	110
CGG CGG AGA TCG CGC AAT CTG GGT AAG GTC ATC GAT ACC CTG ACG TGC		384
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys		
115	120	125
GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC CCC GTC		432
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val		
130	135	140
GGG GGC GTC GCC AGG GCC CTG GCG CAT GGC GTC AGG GCT GTG GAG GAC		480
Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp		
145	150	155
GGG ATT AAC TAT CGA CAG		
Gly Ile Asn Tyr Arg Gln		498
165		

(2) INFORMATION FOR SEQ ID NO: 194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn			
1	5	10	15
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly			
20	25	30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala			
35	40	45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro			
50	55	60	
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Ala Gly			
65	70	75	80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp			
85	90	95	
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro			
100	105	110	
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys			
115	120	125	
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val			
130	135	140	

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp
 145 150 155 160
 Gly Ile Asn Tyr Arg Gln
 165

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

ACG TGC GGA TTC GCC GAC CTC GTG GGG TAC ATC CCG CTC GTA GGC GGC	48
Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly	
1 5 10 15	
CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAT GGT GTG AGG GTT CTT	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu	
20 25 30	
GAG GAC GGG GTG AAT TAT GCA ACA GGG AAT CTG CCT GGT TGC TCT TTC	144
Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC ATT CTT GCA CTT CTC TCG TGC CTC ACT GTC CCG GCC TCT	192
Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCA GTT CCC TAC CGA AAT GCC TCT GGG ATC TAT CAT GTC ACC AAT GAT	240
Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT GAT CTG ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His	
85 90 95	
GCA CCT GGC TGC GTG CCT TGT GTC AGG AAA GAT AAT GTG AGT AGG TGC	336

Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys			
100	105	110	
TGG GTC CAA ATT ACC CCC ACG CTG TCA GCC CCG AGC TTC GGA GCA GTC			384
Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val			
115	120	125	
ACG GCT CCC CTT CGG AGA GCC GTT GAT TAC TTG GTG GGA GGG GCT GCC			432
Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala			
130	135	140	
CTC TGC TCC GCG TTA TAC GTT GGA GAC GCG TGT GGG GCA CTA TTT TTG			480
Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu			
145	150	155	160
GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAT GCT ACG GTG CAG			
Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln			
165	170	175	
GAC TGC AAC TGT TCC ATC TAC AGT GGC CAC GTC ACC GGC CAT CAG ATG			576
Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met			
180	185	190	
GCA			579
Ala			

(2) INFORMATION FOR SEQ ID NO: 196:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly		
1	5	10
		15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu		
20	25	30

Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe.		
35	40	45

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser		
50	55	60

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp		
65	70	75
		80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His		
85	90	95

Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys		
100	105	110

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val
 115 120 125

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala
 130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

48

CCC GTG GGT GGC GTC GCC AGA GCA CTG GAA CAT GGT GTT AGG GCT GTG
 Pro Val Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val
 20 25 30

96

GAG GAC GGC ATC AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTC
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45

144

TCT ATC TAC CTC TTG GCA CTT CTC TCG TGC CTG ACT GTT CCC ACC TCG

192

Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser			
50	55	60	
GCC ATC CAC TAT CGC AAT GCC TCG GGC GTC TAC CAC GTC ACC AAT GAC			240
Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp			
65	70	75	80
TGC CCG AAC TCG AGC ATA GTG TAC GAG GCC GAC CAC CAC ATC CTA CAC			288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His			
85	90	95	
CTT CCA GGG TGC TTA CCC TGT GTG AGG GTT GGG AAT CAG TCA CGT TGT			336
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys			
100	105	110	
TGG GTG GCC CTC TCT CCC ACC GTG GCG GCG CCT TAC ATC GGT GCT CCA			384
Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro			
115	120	125	
GTT GAA TCC TTC CGG AGA CAC GTG GAC ATG ATG GTG GGC GCT GCT ACT			432
Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr			
130	135	140	
GTG TGC TCC GCT CTC TAT ATT GGG GAC TTG TGT GGT GGC GTA TTC TTG			480
Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu			
145	150	155	160
GTT GGT CAG ATG TTT TCT TTC CGG CCA CGA CGC CAC TGG ACT ACG CAG			528
Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln			
165	170	175	
GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC ATC ACT GGC CAC GGA ATG			576
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met			
180	185	190	
GCA			579
Ala			

(2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val
 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe

35

40

45

Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser
50 55 60

Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His
85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys
100 105 110

Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro
115 120 125

Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr
130 135 140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
145 150 155 160

Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1470

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..1467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

A TCA CCA CCG GAG CTT CTA TCA CAT ACT CCA CTT ACG GCA AGT TCC Ser Pro Pro Glu Leu Leu Ser His Thr Pro Leu Thr Ala Ser Ser	46
1 5 10 15	
TTG CTG ATG GAG GGT GTT CAG GCG GCG CGC ATG ACG TGA TCA TAT GCG Leu Leu Met Glu Gly Val Gln Ala Ala Arg Met Thr * Ser Tyr Ala	94
20 25 30	
ACG AGT GCC ATT CCC AGG ACG CCA CCA TTC TTG GGA TAG GCA CTG Thr Ser Ala Ile Pro Arg Thr Pro Pro Phe Leu Gly * Ala Leu	142
35 40 45	
TCC TTG ACC AGG CAG AGA CGG CTG GAG CTA GGC TCG TCG TCT TGG CCA Ser Leu Thr Arg Gln Arg Arg Leu Glu Leu Gly Ser Ser Ser Trp Pro	190
50 55 60	
CGG CCA CCC CTC CCG GCA GTG TGA CAA CGC CCC ACC CCA ACA TCG AGG Arg Pro Pro Leu Pro Ala Val * Gln Arg Pro Thr Pro Thr Ser Arg	238
65 70 75	
AAG TGG CCC TGC CTC AGG AGG GGG AGG TTC CCT TCT ACG GCA GAG CCA Lys Trp Pro Cys Leu Arg Arg Gly Arg Phe Pro Ser Thr Ala Glu Pro	286
80 85 90 95	
TTC CCC TTG CTT TTA TAA AGG GTG GTA GGC ATC TCA TCT TCT GCC ATT Phe Pro Leu Leu Leu * Arg Val Val Gly Ile Ser Ser Ser Ala Ile	334
100 105 110	
CCA AGA AAA AAT GTG ATG AAC TCG CCA AGC AAC TGA CCA GCC TGG GCG Pro Arg Lys Asn Val Met Asn Ser Pro Ser Asn * Pro Ala Trp Ala	382
115 120 125	
TGA ACG CCG TGG CAT ATT ATA GAG GTC TAG ACG TCG CCG TCA TAC CCA * Thr Pro Trp His Ile Ile Glu Val * Thr Ser Pro Ser Tyr Pro	430
130 135 140	
CAA CAG GAG ACG TGG TCG TGT GCA GCA CCG ACG CGC TCA TGA CGG GAT Gln Gln Glu Thr Trp Ser Cys Ala Ala Pro Thr Arg Ser * Arg Asp	478
145 150 155	
TCA CCG GCG ACT TTG ATT CTG TCA TAG ACT GCA ACT CCG CCG TCA CTC Ser Pro Ala Thr Leu Ile Leu Ser * Thr Ala Thr Pro Pro Ser Leu	526
160 165 170 175	
AGA CGG TGG ACT TCA GTC TGG ATC CCA CTT TTA CCA TTG AGA CTA CCA Arg Arg Trp Thr Ser Val Trp Ile Pro Leu Leu Pro Leu Arg Leu Pro	574
180 185 190	
CAG TGC CCC AGG ACG CAG TGT CCA GAA GCC AGC GTT GGG GCC GCA CGG Gln Cys Pro Arg Thr Gln Cys Pro Glu Ala Ser Val Gly Ala Ala Arg	622
195 200 205	
GGA GAG GTA GGC ACG GCA TAT ACC GGT ATG TCT CGG CTG GAG AGA GAC Gly Glu Val Gly Thr Ala Tyr Thr Gly Met Ser Arg Leu Glu Arg Asp	670
210 215 220	
CGT CTG GCA TGT TCG ACT CCG TGG TGC TCT GTG AGT GCT ACG ATG CCG Arg Leu Ala Cys Ser Thr Pro Trp Cys Ser Val Ser Ala Thr Met Pro	718

225	230	235	
GAT GTG CAT GGT ACG ATC TGA CTC CTG CCG AGA CTA CCG TGA GGT TGC Asp Val His Gly Thr Ile * Leu Leu Pro Arg Leu Pro * Gly Cys	240	245	766
250		255	
GCG CTT ACT AAA CAC CCC CGG GCT CCC TGT CTG TCA GGA CCA TTT GGA Ala Leu Thr Lys His Pro Arg Ala Pro Cys Leu Ser Gly Pro Phe Gly	260	265	814
		270	
ATT CTG GGA GGG GGT GTT CAC GGG GCT CAC TAA CAT CGA CGC TCA CAT Ile Leu Gly Gly Val His Gly Ala His * His Arg Arg Ser His	275	280	862
		285	
GCT GTC ACA GAC CAA ACA GGG TGG GGA GAA TTT CCC ATA CCT TGT AGC Ala Val Thr Asp Gln Thr Gly Trp Gly Glu Phe Pro Ile Pro Cys Ser	290	295	910
		300	
GTA CCA AGC AAC AGT CTG TGT TCG CGC GAA AGC GCC CCC CAG CTG Val Pro Ser Asn Ser Leu Cys Ser Arg Glu Ser Ala Pro Pro Gln Leu	305	310	958
		315	
GGA CAC AAT GTG GAA ATG CAT GCT CCG TCT CAA ACC GAC TTA ACT GGC Gly His Asn Val Glu Met His Ala Pro Ser Gln Thr Asp Leu Thr Gly	320	325	1006
		330	335
CCT ACT CCC CTC TTG TAC AGG CTG GGG CCC GTC CAG AAT GAG ATC ACA Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile Thr	340	345	1054
		350	
CTG ACG CAC CCC ATC ACC AAG TAC ATT ATG GCT TGC ATG TCT GCG GAC Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp	355	360	1102
		365	
TTG GAG GTC ATT ACC AGC ACT TGG GTT CTG GTG GGG GGC GTT GTG GCG Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val Ala	370	375	1150
		380	
GCC CTG GCG GCC TAC TGC TTG ACG GTG GGT TCG GTA GCC ATA GTC GGT Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val Gly	385	390	1198
		395	
AGG ATC ATC CTC TCT GGG AAA CCT GCC ATC ATT CCC GAT AGG GAG GTA Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val	400	405	1246
		410	415
TTA TAC CAG CAA TTT GAT GAG ATG GAG GAG TGC TCG GCC TCG TTG CCC Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu Pro	420	425	1294
		430	
TAT ATG GAC GAA ACA CGT GCC ATT GCC GGA CAA TTC AAA GAG AAA GTG Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys Val	435	440	1342
		445	
CTC GGC TTC ATC AGC ACG ACC GGC CAG AAG GCT GAA ACT CTG AAG CCG Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys Pro	450	455	1390
		460	

GCA GCC ACG TCT GTG TGG AAC AAG GCT GAG CAG TTC TGG CCA CAT ACA 1438
 Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Pro His Thr
 465 470 475

TGT GGA ACT TCA TCA GTG GGA TAC AAT AAT AG 1470
 Cys Gly Thr Ser Ser Val Gly Tyr Asn Asn
 480 485

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

TGTGCCAGGA CCATCACCAAC CGGAGCTTCT ATCACATACT CCACTTACGG CAAGTTCCCTT	60
GCTGATGGAG GGTGTTCAAGG CGGCAGCGCAT GACGTGATCA TATGCGACGA GTGCCATTCC	120
CAGGACGCCA CCACCATTCT TGGGATAGGC ACTGTCTTG ACCAGGCAGA GACGGCTGGA	180
GCTAGGCTCG TCGTCTTGGC CACGGCCACC CCTCCCGGCA GTGTGACAAC GCCCCACCCC	240
AACATCGAGG AAGTGGCCCT GCCTCAGGAG GGGGAGGTTC CCTTCTACGG CAGAGCCATT	300
CCCCTTGCTT TTATAAAGGG TGGTAGGCAT CTCATCTTCT GCCATTCCAA GAAAAAATGT	360
GATGAACTCG CCAAGCAACT GACCAGCCTG GGCGTGAACG CCGTGGCATA TTATAGAGGT	420
CTAGACGTCG CCGTCATACC CACAACAGGA GACGTGGTCG TGTGCAGCAC CGACGCGCTC	480
ATGACGGGAT TCACCGGCAGA CTTTGATTCT GTCATAGACT GCAACTCCGC CGTCACTCAG	540
ACGGTGGACT TCAGTCTGGA TCCCACTTTT ACCATTGAGA CTACCACAGT GCCCCAGGAC	600
GCAGTGTCCA GAAGCCAGCG TTGGGGCCGC ACAGGGAGAG GTAGGCACGG CATATACCGG	660
TATGTCTCGG CTGGAGAGAG ACCGTCTGGC ATGTTGACT CCGTGGTGCT CTGTGAGTGC	720
TACGATGCCG GATGTGCATG GTACGATCTG ACTCCTGCCG AGACTACCGT GAGGTTGCAG	780
GCTTACNTAA ACACCCCCGG GCTCCCTGTC TGTCAGGACC ATTTGGAATT CTGGGAGGGG	840
GTGTTCACGG GGCTCACTAA CATCGACGCT CACATGCTGT CACAGACCAA ACAGGGTGGG	900
GAGAATTTCG CATACTTGT AGCGTACCAA GCAACAGTCT GTGTTCGCGC GAAAGCGCCC	960

CCCCCCCAGCT	GGGACACAAT	GTGGAAATGC	ATGCTCCGTC	TCAAACCGAC	NTTAACTGGC	1020
CCTACTCCCC	TCTTGTACAG	GCTGGGGCCC	GTCCAGAATG	AGATCACACT	GACGCACCCC	1080
ATCACCAAGT	ACATTATGGC	TTGCATGTCT	GCGGACTTGG	AGGTCAATTAC	CAGCACTTGG	1140
GTTCTGGTGG	GGGGCGTTGT	GGCGGCCCTG	GCAGGCCTACT	GCTTGACGGT	GGGTTCGGTA	1200
GCCATAGTCG	GTAGGATCAT	CCTCTCTGGG	AAACCTGCCA	TCATTCCCGA	TAGGGAGGTA	1260
TTATACCAGC	AATTGATGA	GATGGAGGAG	TGCTCGGCCT	CGTTGCCCTA	TATGGACGAA	1320
ACACGTGCCA	TTGCCGGACA	ATTCAAAGAG	AAAGTGCTCG	GCTTCATCAG	CACGACCGGC	1380
CAGAAGGCTG	AAACTCTGAA	GCCGGCAGCC	ACGTCTGTGT	GGAACAAGGC	TGAGCAGTTC	1440
TGGNCCACAT	ACATGTGGAA	CTTCATCAGT	GGGATAACAAT	AATAG		1485

(2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 484 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Cys	Ala	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Ser	Ile	Thr	Tyr	Ser	Thr	Tyr
1				5						10				15	
Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	His	Asp	Val
		20							25				30		
Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Gln	Asp	Ala	Thr	Thr	Ile	Leu	Gly
		35						40				45			
Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val
	50				55				60						
Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Thr	Pro	His	Pro
	65				70					75			80		
Asn	Ile	Glu	Glu	Val	Ala	Leu	Pro	Gln	Glu	Gly	Glu	Val	Pro	Phe	Tyr
		85						90					95		
Gly	Arg	Ala	Ile	Pro	Leu	Ala	Phe	Ile	Lys	Gly	Gly	Arg	His	Leu	Ile
		100						105				110			
Phe	Cys	His	Ser	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Lys	Gln	Leu	Thr	
	115					120					125				
Ser	Leu	Gly	Val	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ala
	130					135				140					

Val Ile Pro Thr Thr Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu
145 150 155 160

Met Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser
165 170 175

Ala Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile
180 185 190

Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Trp
195 200 205

Gly Arg Thr Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala
210 215 220

Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Val Val Leu Cys Glu Cys
225 230 235 240

Tyr Asp Ala Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr
245 250 255

Val Arg Leu Arg Ala Tyr Xaa Asn Thr Pro Gly Leu Pro Val Cys Gln
260 265 270

Asp His Leu Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile
275 280 285

Asp Ala His Met Leu Ser Gln Thr Lys Gln Gly Glu Asn Phe Pro
290 295 300

Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro
305 310 315 320

Pro Pro Ser Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro
325 330 335

Xaa Leu Thr Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln
340 345 350

Asn Glu Ile Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys
355 360 365

Met Ser Ala Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly
370 375 380

Gly Val Val Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val
385 390 395 400

Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro
405 410 415

Asp Arg Glu Val Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser
420 425 430

Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe
435 440 445

Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu
 450 455 460

Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe
 465 470 475 480

Trp Xaa Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

TGTGCCAGGA CCATCACCAAC CGGAGCTTCT ATCACATACT CCACTTACGG CAAGTTCCCTT	60
GCTGATGGAG GGTGTTCAAGG CGGCAGCGTAT GACGTGATCA TATGCGACGA GTGCCATTCC	120
CAGGACGCCA CCACCATTCT TGGGATAGGC ACTGTCCCTTG ACCAGGCAGA GACGGCTGGA	180
GCTAGGCTCG TCGTCTTGGC CACGGCCACC CCTCCCGCA GTGTGACAAC GCCCCACCCC	240
AACATCGAGG AAGTGGCCCT GCCTCAGGAG GGGGAGGGTTC CCTTCTACGG CAGAGCCATT	300
CCCCTTGCTT TTATAAAGGG TGGTAGGCAT CTCATCTTCT GCCATTCCAA GAAAAAAATGT	360
GATGAACTCG CCAAGCAACT GACCAGCCTG GGCAGAACG CCGTGGCATA TTATAGAGGT	420
CTAGACGTCG CCGTCATCCC CACAGCAGGA GACGTGGTCG TGTGCAGCAC CGACGCGCTC	480
ATGACGGGAT TCACCGGCCA CTTTGATTCT GTCATAGACT GCAACTCCGC CGTCACTCAG	540
ACGGTGGACT TCAGTCTGGA TCCCACTTTT ACCATTGAGA CTACCACAGT GCCCCAGGAC	600
GCAGTGTCCA GAAGCCAGCG TAGGGGCCGC ACGGGGAGAG GTAGGCACGG CATATACCGG	660
TATGTCTCGG CTGGAGAGAG ACCNTCTGAC ATGTTCGACT CCGTGGTGCT CTGTGAGTGC	720
TACGATGCCG GATGTGCGTG GTATGATCTG ACTCCTGCCG AGACTACCGT GAGGTTGCGC	780
GCTTACATAA ACACCCCCGG GCTCCCTGTC TGTCAGGACC ATTTGGAATT CTGGGAGGGG	840
GTGTTCACGG GGCTCACTAA CATCGACGCT CACATGCTGT CACAGACCAA ACAGGGTGGG	900
GAGAATTTCNC CATAACCTTGT AGCGTACCAA GCAACAGTCT GTGTTCGCGC GAAAGCGCCC	960

CCCCCCCAGCT	GGGACACAAT	GTGGAAATGC	ATGCTCCGTC	TCAAACCGAC	TTTAACCTGGC	1020
CCTACTCCCC	TCTTGTACAG	GCTGGGGCCC	GTCCAGANTG	AGATCACACT	GACGCACCCC	1080
ATCACCAAGT	ACATTATGGC	TTGCATGTCT	GCGGACTTGG	AGGTCAATTAC	CANCACTTGG	1140
GTTCTGGTGG	GGGGCGTTGT	GGCGGCCCTG	GC GG CCTACT	GCTTGACGGT	GGGTTCGGTA	1200
GCCATAGTCG	GTAGGATCAT	CCTCTCTGGG	AAACCTGCCA	TCATTCCCGA	TAGGGAGGCA	1260
TTATACCAGC	AATTTGATGA	GATGGAGGAG	TGCTCGGCCT	CGTTGCCCTA	TATGGACGAG	1320
ACACGTGCCA	TTGCCGGACA	ATTCAAAGAG	AAAGTGCTCG	GCTTCATCAG	CACGACCGGC	1380
CAGAAGGCTG	AAACTCTGAA	GCCGGCAGCC	ACGTCTGTGT	GGAACAAGGC	TGAGCAGTTC	1440
TGGGCCACAT	ACATGTGGAA	CTTCATCAGC	GGGATAACAAT	AATAG		1485

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

Cys	Ala	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Ser	Ile	Thr	Tyr	Ser	Thr	Tyr
1				5						10				15	

Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Val
						20			25				30		

Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Gln	Asp	Ala	Thr	Thr	Ile	Leu	Gly
						35		40				45			

Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val
					50		55			60					

Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Thr	Pro	His	Pro
65					70				75			80			

Asn	Ile	Glu	Glu	Val	Ala	Leu	Pro	Gln	Glu	Gly	Glu	Val	Pro	Phe	Tyr
						85			90			95			

Gly	Arg	Ala	Ile	Pro	Leu	Ala	Phe	Ile	Lys	Gly	Gly	Arg	His	Leu	Ile
						100			105			110			

Phe	Cys	His	Ser	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Lys	Gln	Leu	Thr	
						115			120			125			

Ser Leu Gly Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala
 130 135 140
 Val Ile Pro Thr Ala Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu
 145 150 155 160
 Met Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser
 165 170 175
 Ala Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile
 180 185 190
 Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg
 195 200 205
 Gly Arg Thr Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala
 210 215 220
 Gly Glu Arg Xaa Ser Asp Met Phe Asp Ser Val Val Leu Cys Glu Cys
 225 230 235 240
 Tyr Asp Ala Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr
 245 250 255
 Val Arg Leu Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln
 260 265 270
 Asp His Leu Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile
 275 280 285
 Asp Ala His Met Leu Ser Gln Thr Lys Gln Gly Glu Asn Xaa Pro
 290 295 300
 Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro
 305 310 315 320
 Pro Pro Ser Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro
 325 330 335
 Thr Leu Thr Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln
 340 345 350
 Xaa Glu Ile Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys
 355 360 365
 Met Ser Ala Asp Leu Glu Val Ile Thr Xaa Thr Trp Val Leu Val Gly
 370 375 380
 Gly Val Val Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val
 385 390 395 400
 Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro
 405 410 415
 Asp Arg Glu Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser
 420 425 430
 Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe

435

440

445

Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu
 450 455 460

Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe
 465 470 475 480

Trp Ala Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(x) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

C TCC ACT GTG ACT GAG AGA GAC ATC AGG GTC GAA GAA GAA GTC TAT	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr	
1 5 10 15	

CAG TGT TGT GAT CTG GAG CCC GAG GCC CGC AAG GTA ATA ACC GCC CTC	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu	
20 25 30	

ACG GAG AGA CTC TAC GTG GGC GGC CCT ATG TAC AAT AGC AAG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp	
35 40 45	

CTT TGC GGG TAT CGC AGG TGC CGC GCA AGC GGC GTA TAT ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	

TTC GGG AAC ACA CTG ACG TGC TAC CTT AAA GCC TCA GCA GCC ATC AGG	238
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg	
65 70 75	

GCT GCG GGG CTG AAG GAC TGC ACC ATG CTG GTT TGC GGT GAC GAC TTA	286
Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	

GTC GTG ATC GCT GAA AGC GGT GGC GTC GAG GAG GAC AAG CGA GCC CTC 334
 Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu
 100 105 110

GGA GCT 340
Gly Ala

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
 50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
 65 70 75 80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

C TCC ACA GTG ACT GAA AGA GAC ATC AGG GTC GAG GAA GAG GTC TAC Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr	46
1 5 10 15	
CAG TGT TGT GAC CTG GAG CCT GAA ACC CGC AAG GTA ATA TCT GCC CTC Gln Cys Cys Asp Leu Glu Pro Glu Thr Arg Lys Val Ile Ser Ala Leu	94
20 25 30	
ACT GAA AGA CTC TAT GTG GGC GGT CCC ATG CAC AAC AGC AGG GGA GAC Thr Glu Arg Leu Tyr Val Gly Pro Met His Asn Ser Arg Gly Asp	142
35 40 45	
CTA TGC GGG TAC CGT AGA TGC CGC GCG AGC GGC GTA TAC ACC ACA AGC Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	190
50 55 60	
TTC GGG AAC ACT CTG ACG TGC TTC CTC AAG GCC ACA GCG GCC ACC AAA Phe Gly Asn Thr Leu Thr Cys Phe Leu Lys Ala Thr Ala Ala Thr Lys	238
65 70 75	
GCC GCT GGC CTA AAG GAC TGC ACC ATG TTG GTG TGT GGT GAC GAC TTA Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	286
80 85 90 95	
GTC GTT ATC GCC GAA AGC GAT GGT GTC GAA GAG GAC CGC CGA GCC CTC Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Arg Arg Ala Leu	334
100 105 110	
GGA GCT Gly Ala	340

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln	
1 5 10 15	

Cys Cys Asp Leu Glu Pro Glu Thr Arg Lys Val Ile Ser Ala Leu Thr
 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp Leu
 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
 50 55 60

Gly Asn Thr Leu Thr Cys Phe Leu Lys Ala Thr Ala Ala Thr Lys Ala
 65 70 75 80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Arg Arg Ala Leu Gly
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(x) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

C TCC ACG GTG ACC GAA AGG GAT ATC AGG ACC GAG GAA GAG ATC TAC Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr	46
1 5 10 15	

CAG TGC TGC GAC CTG GAG CCC GAA GCC CGC AAG GTG ATA TCC GCC CTA Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu	94
20 25 30	

ACG GAA AGA CTC TAC GTG GGC GGT CCC ATG TAC AAC TCC AAG GGG GAC Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp	142
35 40 45	

09899046 - 070604

CTA TGC GGG CAA CGG AGG TGC CGC GCA AGC GGG GTC TAC ACC ACC AGC Leu Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser 50 55 60	190
TTC GGG AAC ACT GTA ACG TGT TAT CTC AAG GCC GTT GCG GCT ACT AGG Phe Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg 65 70 75	238
GCC GCA GGT CTG AAA GGT TGC AGC ATG CTG GTT TGT GGA GAC GAC TTA Ala Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu 80 85 90 95	286
GTC GTC ATC TGC GAG AGC GGC GGC GTA GAG GAG GAT GCA AGA GCC CTC Val Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu 100 105 110	334
CGA GCC Arg Ala	340

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr Gln 1 5 10 15
Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr 20 25 30
Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu 35 40 45
Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe 50 55 60
Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg Ala 65 70 75 80
Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val 85 90 95
Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

C TCC ACG GTG ACT GAA AGG GAC ATT AGG GTC GAG GAA GAG ATC TAC	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Ile Tyr	
1 5 10 15	
CAG TGC TGT GAC CTG GAG CCC GAG GCA CGC AAG GTG ATA TCC GCT CTC	94
Gln Cys Cys Asp Leu Glu Pro Ala Arg Lys Val Ile Ser Ala Leu	
20 25 30	
ACA GAA AGA CTC TAC AAG GGC GGC CCC ATG TAT AAC AGC AAG GGG GAC	142
Thr Glu Arg Leu Tyr Lys Gly Pro Met Tyr Asn Ser Lys Gly Asp	
35 40 45	
CTA TGC GGG CTT CGG AGG TGC CGC GCA AGC GGG GTA TAC ACC ACA AGC	190
Leu Cys Gly Leu Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACG GTG ACA TGC TAC CTT AAA GCC ACA GCA GCC ACC AGG	238
Phe Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg	
65 70 75	
GCT GCA GGG CTG AAA GAT TGC ACT ATG CTG GTA TGC GGT GAC GAC TTA	286
Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTC GTT ATT GCC GAA AGC GGT GGC GTG GAG GAG GAC GCC CGA GCC CTC	334
Val Val Ile Ala Glu Ser Gly Val Glu Glu Asp Ala Arg Ala Leu	
100 105 110	
CGA GCC	340
Arg Ala	

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Val	Glu	Glu	Glu	Ile	Tyr	Gln
1									10						15

Cys	Cys	Asp	Leu	Glu	Pro	Glu	Ala	Arg	Lys	Val	Ile	Ser	Ala	Leu	Thr
									25					30	

Glu	Arg	Leu	Tyr	Lys	Gly	Gly	Pro	Met	Tyr	Asn	Ser	Lys	Gly	Asp	Leu
									40				45		

Cys	Gly	Leu	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Tyr	Thr	Thr	Ser	Phe
									55				60		

Gly	Asn	Thr	Val	Thr	Cys	Tyr	Leu	Lys	Ala	Thr	Ala	Ala	Thr	Arg	Ala
									65			75		80	

Ala	Gly	Leu	Lys	Asp	Cys	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val
									85			90		95	

Val	Ile	Ala	Glu	Ser	Gly	Gly	Val	Glu	Glu	Asp	Ala	Arg	Ala	Leu	Arg
									100			105		110	

Ala

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

CCCCACCGTG	ACNGAGAGGG	ACNTCAGGGT	CGAGGAAGAG	GTCTATCAGT	GCTGTAATCT	60
------------	------------	------------	------------	------------	------------	----

GGAGNCCGAT	GNCCGCAAGG	TCATCACAGC	CCTCACAGAG	AGACTCTACG	TGGGCGGCCC	120
------------	------------	------------	------------	------------	------------	-----

TATGCACAAC AGCAAGGGAG ACCTGTGTGG CATCCGTAGA TGCCGCGCGA GCGGCCTTTA	180
CACCACGAGC TTGGAAACA CGCTGACTTG CTACCTCAA GCCACAGCGG CCACCAGGGC	240
CGCGGGCTTG AAGGATTGCA CCATGCTGGT CTGCGGNAC GACCTGGTTG TCATTGCTGA	300
GAGCATTGGC ATAGACGAGG ACAAGCAAGC CCTCCGNACT	340

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

Pro	Thr	Val	Thr	Glu	Arg	Asp	Xaa	Arg	Val	Glu	Glu	Glu	Val	Tyr	Gln
1															
															15

Cys	Cys	Asn	Leu	Glu	Xaa	Asp	Xaa	Arg	Lys	Val	Ile	Asn	Ala	Leu	Thr
															30
20															

Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	His	Asn	Ser	Lys	Gly	Asp	Leu
35															45

Cys	Gly	Ile	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Tyr	Thr	Thr	Ser	Phe
50															60

Gly	Asn	Thr	Leu	Thr	Cys	Tyr	Leu	Lys	Ala	Thr	Ala	Ala	Thr	Arg	Ala
65															80

Ala	Gly	Leu	Lys	Asp	Cys	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val
85															95

Val	Ile	Ala	Glu	Ser	Ile	Gly	Ile	Asp	Glu	Asp	Lys	Gln	Ala	Leu	Arg
100															110

Thr

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

CTCGACTGTG NCCGAGAGGG ACATCAGGAC AGAGGGAGAG GTCTATCACT GTTGCACCT	60
GGAAACCGGAA GCCCGCAAGG TAATCACCGC CCTCACTGAG AGACTCTATG TGGGCGGACC	120
CATGTTAAC AGCAAGGGAG ACCTGTGCGG ACAACGCCGG TGCCGCGCAA GCGGCGTGT	180
CACCACCAGC TTCGGGAACA CACTGACGTG CTACCTTAAA GCCACAGCTG CTACTAGAGC	240
AGCCGGCTTA AAAGATTGCA CCATGCTGGT CTGCGGTGAC GACTTAGTCG TTATTTCCGA	300
GAGCGCCGGT GTGGAGGAGG ATCCCANAAC CNNNCGACCN	340

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

Ser Thr Val Xaa Glu Arg Asp Ile Arg Thr Glu Gly Glu Val Tyr Gln			
1	5	10	15
10	15		

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr			
20	25	30	
30			

Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly Asp Leu			
35	40	45	
45			

Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Phe			
50	55	60	
60			

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala

65	70	75	80
Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val			
85	90	95	
Val Ile Ser Glu Ser Ala Gly Val Glu Glu Asp Pro Xaa Thr Xaa Arg			
100	105	110	

(2) INFORMATION FOR SEO ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2...340

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

C TCA ACA GTC ACC GAG AAC GAC ATC CGT GTT GAG GAG TCA ATT TAC	46
Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr	
1 5 10 15	

CAA TGT TGT GAC TTG GCC CCC GAG GCC AGA CAG GCC ATA AAG TCG CTC
 Gln Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser Leu
 20 25 30

ACA GAG CGG CTT TAT ATC GGG GGT CCC CTG ACT AAT TCA AAG GGG CAG 142
 Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln
 35 40 45

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AAC TGT GGC TAT CGC CGA TGC CGC GCA AGC GGC GTG CTG ACG ACC AGC 190
Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser
      50          55          60

```

TGC GGT AAT ACC CTT ACA TGT TAC CTA AAG GCC TCT GCA GCC TGT CGA 238
 Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg
 65 70 75

GCT GCG AAG CTC CAG GAC TGC ACG ATG CTC GTG TGC GGG GAC GAC CTT 286

Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Asp Leu
 80 85 90 95

GTC GTT ATC TGT GAA AGC GCG GGA ACC CAA GAG GAC GCG GCG AGC CTA 334
 Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu
 100 105 110

CGA GTC
Arg Val 340

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr Gln
1 5 10 15

Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser Leu Thr
 20 25 30

Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg Ala
65 70 75 80

Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Asp Leu Val
85 90 95

Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu Arg
100 105 110

val

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

C TCA ACC GTC ACG GAG AGG GAT ATA AGA ACA GAA GAA TCC ATA TAT Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr	46
1 5 10 15	
CAA GCT TGT TCC CTG CCC CAA GAG GCC AGA ACT GTC ATA CAC TCG CTC Gln Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu	94
20 25 30	
ACC GAG AGA CTC TAC GTG GGA GGG CCC ATG ATA AAC AGC AAA GGG CAA Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Ile Asn Ser Lys Gly Gln	142
35 40 45	
TCC TGC GGT TAC AGG CGT TGC CGC GCA AGC GGT GTT TTC ACC ACC AGC Ser Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser	190
50 55 60	
ATG GGG AAT ACC ATG ACG TGT TAC ATC AAA GCC CTT GCA GCG TGT AAA Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys	238
65 70 75	
GCC GCA GGG ATC GTG GAC CCC GTC ATG CTG GTG TGT GGA GAC GAC CTG Ala Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu	286
80 85 90 95	
GTC GTC ATC TCG GAG AGC CAG GGT AAC GAG GAG GAC GAG CGA AAC CTG Val Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn Leu	334
100 105 110	
AGA GCT Arg Ala	340

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln
1 5 10 15

Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Ile Asn Ser Lys Gly Gln Ser
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met
50 55 60

Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys Ala
65 70 75 80

Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ser Glu Ser Gln Gly Asn Glu Asp Glu Arg Asn Leu Arg
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

C TCG ACT GTC ACT GAA CAG GAC ATC AGG GTG GAA GAG GAG ATA TAT 46
Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr
1 5 10 15

CAA TGC TGC AAC CTT GAA CCG GAG GCC AGG AAA GTG ATC TCC TCC CTC 94
Gln Cys Cys Asn Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ser Leu

20

25

30

ACG GAG CGG CTT TAC TGC GGA GGC CCT ATG TTT AAC AGC AAG GGG GCC	142
Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Ala	
35 40	45
 CAG TGT GGT TAT CGC CGT TGC CGT GCC AGT GGA GTT CTG CCT ACC AGC	190
Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser	
50 55	60
 TTT GGC AAC ACA ATC ACT TGT TAC ATC AAG GCC ACA ACG GCC GCG AAG	238
Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Thr Ala Ala Lys	
65 70	75
 GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTC TGC GGA GAT GAT CTG	286
Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp Leu	
80 85	90 95
GTC GTG GTG GCT GAG AGT GAT GGC GTC GAC GAG GAT AGA GCA GCC CTG	334
Val Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Ala Ala Leu	
100 105	110
 AGA GCC	340
Arg Ala	

(2) INFORMATION FOR SEQ ID NO: 218:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln
 1 5 10 15

Cys Cys Asn Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ser Leu Thr
 20 25 30

Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Ala Gln
 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe
 50 55 60

Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Thr Ala Ala Lys Ala
 65 70 75 80

Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp Leu Val
 85 90 95

Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Ala Ala Leu Arg
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

Arg Ser Glu Gly Arg Thr Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

Arg Ser Glu Gly Arg Thr Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

Arg Thr Glu Gly Arg Thr Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 629 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 3..629

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 3..629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

TA GAC TTT TGG GAG AGC GTC TTC ACT GGA CTA ACT CAC ATA GAT GCC	47
Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala	
1 5 10 15	
CAC TTT CTG TCA CAG ACT AAG CAG CAG GGA CTC AAC TTC TCG TTC CTG	95
His Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu	
20 25 30	
ACT GCC TAC CAA GCC ACT GTG TGC GCT CGC GCG CAG GCT CCT CCC CCA	143
Thr Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro	
35 40 45	
AGT TGG GAC GAG ATG TGG AAG TGT CTC GTA CGG CTT AAG CCA ACA CTA	191
Ser Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu	
50 55 60	
CAT GGA CCT ACG CCT CTT CTA TAT CGG TTG GGG CCT GTC CAA AAT GAA	239
His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu	
65 70 75	
ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG GCA TGC ATG TCA	287
Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser	
80 85 90 95	
GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG CTT GGA GGG GTC	335
Ala Asp Leu Glu Val Thr Ser Thr Trp Val Leu Leu Gly Gly Val	
100 105 110	
CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT TGT GTT GTG ATT	383
Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys Val Val Ile	
115 120 125	
GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC GTT CCA GAC AAA	431
Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys	
130 135 140	

0908990046 - 09206004

GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG TGC TCA CAA GCT Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys Ser Gln Ala 145 150 155	479
GCC CCA TAT ATC GAA CAA GCT CAG GTA ATA GCT CAC CAG TTC AAG GAA Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln Phe Lys Glu 160 165 170 175	527
AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA CAA GCT GTC ATT Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln Ala Val Ile 180 185 190	575
GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG GCC TTT TGG CAC Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala Phe Trp His 195 200 205	623
AAG CAT Lys His	629

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His 1 5 10 15
Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu Thr 20 25 30
Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser 35 40 45
Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu His 50 55 60
Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile 65 70 75 80
Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala 85 90 95
Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu Gly Gly Val Leu 100 105 110
Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys Val Val Ile Val 115 120 125
Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys Glu 130 135 140

00000000000000000000000000000000

Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys Ser Gln Ala Ala
145 150 155 160

Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln Phe Lys Glu Lys
165 170 175

Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln Ala Val Ile Glu
180 185 190

Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala Phe Trp His Lys
195 200 205

His

(2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 2..12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

Ile His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

02090200-02090200-02090200-02090200-02090200

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

Val Asn Tyr His Asn Thr Ser Gly Ile Tyr His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

Ile His Tyr Arg Asn Ala Ser Asp Gly Tyr Tyr Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

Leu Gln Val Lys Asn Thr Ser Ser Ser Tyr Met Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

Val Trp Gln Leu Arg Ala Ile Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

Val Tyr Glu Ala Asp Tyr His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

Val Tyr Glu Thr Asp Asn His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

Val Tyr Glu Thr Glu Asn His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

Val Phe Glu Thr Val His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

Val Phe Glu Thr Glu His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

Val Phe Glu Thr Asp His His Ile Met His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

Val Tyr Glu Thr Glu Asn His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

Val Tyr Glu Ala Asp Ala Leu Ile Leu His Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

Val Gln Asp Gly Asn Thr Ser Ala Cys Trp Thr Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

Val Arg Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Ile Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Ile Ala Leu

1

5

10

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

Val	Lys	Thr	Gly	Asn	Ser	Val	Arg	Cys	Trp	Ile	Pro	Leu
1						5					10	

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

Val	Lys	Thr	Gly	Asn	Val	Ser	Arg	Cys	Trp	Ile	Ser	Leu
1					5					10		

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

Val	Arg	Lys	Asp	Asn	Val	Ser	Arg	Cys	Trp	Val	Gln	Ile
1					5					10		

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

Ala Pro Ser Phe Gly Ala Val Thr Ala Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

Val Ser Gln Pro Gly Ala Leu Thr Lys Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

Val Lys Tyr Val Gly Ala Thr Thr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

Ala Pro Tyr Ile Gly Ala Pro Val Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

Ala Gln His Leu Asn Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

Ser Pro Tyr Val Gly Ala Pro Leu Glu Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

Ser Pro Tyr Ala Gly Ala Pro Leu Glu Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Ala Pro Tyr Leu Gly Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

Ala Pro Tyr Leu Gly Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

Ala Pro Tyr Val Gly Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Asn Val Pro Tyr Leu Gly Ala Pro Leu Thr Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Ala Pro His Leu Arg Ala Pro Leu Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Ala Pro Tyr Leu Gly Ala Pro Leu Thr Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

Arg Pro Arg Gln His Ala Thr Val Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

Ser Pro Gln His His Lys Phe Val Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

Arg Pro Arg Arg Leu Trp Thr Thr Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

Pro Pro Arg Ile His Glu Thr Thr Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

093290146 10270601

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

Thr Ile Ser Tyr Ala Asn Gly Ser Gly Pro Ser Asp Asp Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

Ser Arg Arg Gln Pro Ile Pro Arg Ala Arg Arg Thr Glu Gly Arg Ser
1 5 10 15

Trp Ala Gln

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1443

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

ACC ATC ACC ACC GGA GCT TCT ATC ACA TAC TCC ACT TAC GGC AAG TTC
Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe

1	5	10	15	
CTT GCT GAT GGA GGG TGT TCA GGC GGC GCG TAT GAC GTG ATC ATA TGC Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys				96
20	25	30		
GAC GAG TGC CAT TCC CAG GAC GCC ACC ACC ATT CTT GGG ATA GGC ACT Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr				144
35	40	45		
GTC CTT GAC CAG GCA GAG ACG GCT GGA GCT AGG CTC GTC GTC TTG GCC Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala				192
50	55	60		
ACG GCC ACC CCT CCC GGC AGT GTG ACA ACG CCC CAC CCC AAC ATC GAG Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu				240
65	70	75	80	
GAA GTG GCC CTG CCT CAG GAG GGG GAG GTT CCC TTC TAC GGC AGA GCC Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala				288
85	90	95		
ATT CCC CTT GCT TTT ATA AAG GGT GGT AGG CAT CTC ATC TTC TGC CAT Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His				336
100	105	110		
TCC AAG AAA AAA TGT GAT GAA CTC GCC AAG CAA CTG ACC AGC CTG GGC Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr Ser Leu Gly				384
115	120	125		
GTG AAC GCC GTG GCA TAT TAT AGA GGT CTA GAC GTC GCC GTC ATC CCC Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala Val Ile Pro				432
130	135	140		
ACA GCA GGA GAC GTG GTC GTG TGC AGC ACC GAC GCG CTC ATG ACG GGA Thr Ala Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu Met Thr Gly				480
145	150	155	160	
TTC ACC GGC GAC TTT GAT TCT GTC ATA GAC TGC AAC TCC GCC GTC ACT Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser Ala Val Thr				528
165	170	175		
CAG ACG GTG GAC TTC AGT CTG GAT CCC ACT TTT ACC ATT GAG ACT ACC Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr				576
180	185	190		
ACA GTG CCC CAG GAC GCA GTG TCC AGA AGC CAG CGT AGG GGC CGC ACG Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr				624
195	200	205		
GGG AGA GGT AGG CAC GGC ATA TAC CGG TAT GTC TCG GCT GGA GAG AGA Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala Gly Glu Arg				672
210	215	220		
CCG TCT GAC ATG TTC GAC TCC GTG GTG CTC TGT GAG TGC TAC GAT GCC Pro Ser Asp Met Phe Asp Ser Val Val Leu Cys Glu Cys Tyr Asp Ala				720
225	230	235	240	

GGA TGT GCG TGG TAT GAT CTG ACT CCT GCC GAG ACT ACC GTG AGG TTG Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr Val Arg Leu 245 250 255	768
CGC GCT TAC ATA AAC ACC CCC GGG CTC CCT GTC TGT CAG GAC CAT TTG Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu 260 265 270	816
GAA TTC TGG GAG GGG GTG TTC ACG GGG CTC ACT AAC ATC GAC GCT CAC Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile Asp Ala His 275 280 285	864
ATG CTG TCA CAG ACC AAA CAG GGT GGG GAG AAT TTC CCA TAC CTT GTA Met Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Phe Pro Tyr Leu Val 290 295 300	912
GCG TAC CAA GCA ACA GTC TGT GTT CGC GCG AAA GCG CCC CCC CCC AGC Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro Pro Pro Ser 305 310 315 320	960
TGG GAC ACA ATG TGG AAA TGC ATG CTC CGT CTC AAA CCG ACT TTA ACT Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro Thr Leu Thr 325 330 335	1008
GGC CCT ACT CCC CTC TTG TAC AGG CTG GGG CCC GTC CAG AAT GAG ATC Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile 340 345 350	1056
ACA CTG ACG CAC CCC ATC ACC AAG TAC ATT ATG GCT TGC ATG TCT GCG Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala 355 360 365	1104
GAC TTG GAG GTC ATT ACC AGC ACT TGG GTT CTG GTG GGG GGC GTT GTG Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val 370 375 380	1152
GCG GCC CTG GCG GCC TAC TGC TTG ACG GTG GGT TCG GTA GCC ATA GTC Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val 385 390 395 400	1200
GGT AGG ATC ATC CTC TCT GGG AAA CCT GCC ATC ATT CCC GAT AGG GAG Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu 405 410 415	1248
GCA TTA TAC CAG CAA TTT GAT GAG ATG GAG GAG TGC TCG GCC TCG TTG Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu 420 425 430	1296
CCC TAT ATG GAC GAG ACA CGT GCC ATT GCC GGA CAA TTC AAA GAG AAA Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys 435 440 445	1344
GTG CTC GGC TTC ATC AGC ACG ACC GGC CAG AAG GCT GAA ACT CTG AAG Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys 450 455 460	1392
CCG GCA GCC ACG TCT GTG TGG AAC AAG GCT GAG CAG TTC TGG GCC ACA Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Ala Thr 465 470 475 480	1440

TAC
Tyr

1443

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

Thr	Ile	Thr	Thr	Gly	Ala	Ser	Ile	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	
1				5						10				15		
Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Val	Ile	Ile	Cys	
				20				25					30			
Asp	Glu	Cys	His	Ser	Gln	Asp	Ala	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr	
	35					40						45				
Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala	
	50				55				60							
Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Thr	Pro	His	Pro	Asn	Ile	Glu	
65					70				75				80			
Gl	u	Val	Ala	Leu	Pro	Gln	Glu	Gly	Glu	Val	Pro	Phe	Tyr	Gly	Arg	Ala
	85					90						95				
Ile	Pro	Leu	Ala	Phe	Ile	Lys	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His	
	100					105				110						
Ser	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Lys	Gln	Leu	Thr	Ser	Leu	Gly		
	115					120				125						
Val	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ala	Val	Ile	Pro	
	130					135					140					
Thr	Ala	Gly	Asp	Val	Val	Val	Cys	Ser	Thr	Asp	Ala	Leu	Met	Thr	Gly	
145					150				155				160			
Phe	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Ser	Ala	Val	Thr	
	165					170						175				
Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr	
	180					185						190				
Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr	
	195					200					205					
Gly	Arg	Gly	Arg	His	Gly	Ile	Tyr	Arg	Tyr	Val	Ser	Ala	Gly	Glu	Arg	
	210				215						220					
Pro	Ser	Asp	Met	Phe	Asp	Ser	Val	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala	

225

230

235

240

Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr Val Arg Leu
245 250 255

Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu
260 265 270

Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile Asp Ala His
275 280 285

Met Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Phe Pro Tyr Leu Val
290 295 300

Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro Pro Pro Ser
305 310 315 320

Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro Thr Leu Thr
325 330 335

Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile
340 345 350

Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala
355 360 365

Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val
370 375 380

Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val
385 390 395 400

Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu
405 410 415

Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu
420 425 430

Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys
435 440 445

Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys
450 455 460

Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Ala Thr
465 470 475 480

Tyr